GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 21:06:58 ; Search time 6604 Seconds
(without alignments)
6530.155 Million cell updates/sec

Title: US-10-036-214-60
Perfect score: 890
Sequence: 1 aagtacttgtgtccgggtgg.....taaaaaaaaaaatcatcaaa 890

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	890	100.0	890	6	AX358978	AX358978 Sequence
2	890	100.0	890	6	AX362471	AX362471 Sequence
3	890	100.0	890	6	AX454720	AX454720 Sequence
4	890	100.0	890	6	AX491198	AX491198 Sequence
5	890	100.0	890	9	AY359109	AY359109 Homo sapi
6	878.2	98.7	914	9	BC020779	BC020779 Homo sapi
7	865.2	97.2	932	6	AX060293	AX060293 Sequence
8	857.8	96.4	897	6	AX083422	AX083422 Sequence
9	833.2	93.6	1028	6	BD248885	BD248885 47 human
10	801.8	90.1	952	6	BD248890	BD248890 47 human
11	783.8	88.1	826	6	BD139366	BD139366 Extended
12	783.8	88.1	826	6	BD203800	BD203800 5'EST and
13	783.8	88.1	826	6	AR412374	AR412374 Sequence
14	783.8	88.1	826	6	AX884144	AX884144 Sequence
15	783.8	88.1	826	6	AX969204	AX969204 Sequence
16	783.8	88.1	826	6	BD023758	BD023758 Sequence
17	783.8	88.1	826	6	BD107927	BD107927 EST and e
18	664.2	74.6	681	6	AX083412	AX083412 Sequence
19	433	48.7	447	6	BD076929	BD076929 5' EST of
c 20	330	37.1	352	11	G27363	G27363 human STS S
c 21	284.2	31.9	138388	9	AC055854	AC055854 Homo sapi
22	269	30.2	269	6	CQ715147	CQ715147 Sequence
23	259.4	29.1	87734	9	AC105046	AC105046 Homo sapi
24	217	24.4	861	6	CQ746667	CQ746667 Sequence
25	200.6	22.5	201	11	BV203131	BV203131 sqnm21113
c 26	164.2	18.4	303	6	AX284030	AX284030 Sequence
c 27	140	15.7	163147	9	AC037441	AC037441 Homo sapi
c 28	140	15.7	171665	2	AC084081	AC084081 Homo sapi
29	138.4	15.6	71310	9	AC134389	AC134389 Homo sapi
30	133	14.9	1031	5	BX931846	BX931846 Gallus ga
c 31	129.4	14.5	62747	2	AC135182	AC135182 Homo sapi
32	105.2	11.8	219	6	CQ746672	CQ746672 Sequence
33	98	11.0	978	5	BC078524	BC078524 Xenopus l
34	83.4	9.4	204545	2	AC108566	AC108566 Rattus no
c 35	83.4	9.4	270725	2	AC126948	AC126948 Rattus no
36	80.6	9.1	724	10	BC048621	BC048621 Mus muscu
c 37	78.6	8.8	603	11	G77998	G77998 S208P6004FE
38	78.6	8.8	110000	2	AC151836_3	Continuation (4 of
39	78.6	8.8	202916	10	AC125151	AC125151 Mus muscu
40	73.4	8.2	871	5	BX934629	BX934629 Gallus ga
c 41	68.4	7.7	239570	2	AC111804	AC111804 Rattus no
42	61.4	6.9	110000	2	AC151836_0	AC151836 Mus muscu
43	61.4	6.9	216834	10	AC123867	AC123867 Mus muscu
c 44	58	6.5	568	11	G83483	G83483 S208P6703FE
45	51	5.7	85063	2	AC151836_4	Continuation (5 of
46	48.8	5.5	1248	3	AY187040	AY187040 Anopheles
47	48.2	5.4	1191	6	CQ855006	CQ855006 Sequence
48	48.2	5.4	1191	6	AX478007	AX478007 Sequence
49	48	5.4	125020	9	AF429315	AF429315 Homo sapi
50	47.2	5.3	1078	6	CQ854996	CQ854996 Sequence
51	47.2	5.3	1078	6	AX477997	AX477997 Sequence
52	47	5.3	686	6	AX525598	AX525598 Sequence
53	47	5.3	1037	10	RNPBP	X71873 R.norvegicu
54	47	5.3	1047	6	E05646	E05646 cDNA encodi
55	47	5.3	1075	10	RNPEABP	X75253 R.norvegicu
56	47	5.3	1105	10	BC063171	BC063171 Rattus no
c 57	46.6	5.2	110000	2	AC151836_0	AC151836 Mus muscu
c 58	46.4	5.2	125020	9	AF429315	AF429315 Homo sapi
59	46.2	5.2	886	6	CQ855032	CQ855032 Sequence
60	46.2	5.2	886	6	AX478033	AX478033 Sequence
61	46.2	5.2	886	8	BT009051	BT009051 Triticum
62	45.8	5.1	1205	10	AF226629	AF226629 Rattus no
63	45.8	5.1	237845	2	AC112433	AC112433 Rattus no
64	45.8	5.1	246867	2	AC111846	AC111846 Rattus no
65	45.4	5.1	847	6	BD160909	BD160909 Gene Hd3a
66	45.4	5.1	847	6	BD160910	BD160910 Gene Hd3a
67	45.4	5.1	847	6	BD169089	BD169089 Gene Hd3a
68	45.4	5.1	847	6	BD169090	BD169090 Gene Hd3a
69	45.4	5.1	847	8	AB052943	AB052943 Oryza sat
70	45.4	5.1	847	8	AB052944	AB052944 Oryza sat
71	43.8	4.9	525	8	AB110009	AB110009 Populus n
72	43.8	4.9	525	8	AB161107	AB161107 Populus n
73	43.2	4.9	770	6	CQ598659	CQ598659 Sequence
74	43.2	4.9	782	3	AY075337	AY075337 Drosophil
c 75	43.2	4.9	2654	6	CQ572912	CQ572912 Sequence
c 76	43.2	4.9	3051	6	CQ598658	CQ598658 Sequence
c 77	43.2	4.9	82631	2	AC020316	AC020316 Drosophil
78	43.2	4.9	145952	3	AE003675	AE003675 Drosophil
c 79	43.2	4.9	157141	3	AC016445	AC016445 Drosophil
c 80	42.8	4.8	2730	6	CQ594011	CQ594011 Sequence
81	42.6	4.8	1238	8	AK072979	AK072979 Oryza sat
82	42.2	4.7	525	8	AB110612	AB110612 Populus n
83	41	4.6	564	6	E09005	E09005 Human cDNA
84	41	4.6	570	9	HSRNAPBP	X85033 H.sapiens m
85	41	4.6	723	9	S76773	S76773 neuropolype
86	41	4.6	1001	6	E09006	E09006 Human cDNA
87	41	4.6	1070	9	BC008714	BC008714 Homo sapi
88	41	4.6	1079	6	AX399866	AX399866 Sequence
89	41	4.6	1364	9	BC017396	BC017396 Homo sapi
90	41	4.6	1434	9	HUMHRPBP	D16111 Homo sapien
91	41	4.6	1442	6	CQ727488	CQ727488 Sequence
92	41	4.6	1444	6	AX411146	AX411146 Sequence

	93	41	4.6	1444	9	HSPEABP	X75252 H.sapiens p
	94	41	4.6	1447	6	E05647	E05647 cDNA encodi
	95	41	4.6	1450	9	BC031102	BC031102 Homo sapi
c	96	41	4.6	1487	11	BV177382	BV177382 sqnm94324
	97	41	4.6	1732	6	CQ497591	CQ497591 Sequence
	98	40.8	4.6	837	6	CQ855004	CQ855004 Sequence
	99	40.8	4.6	837	6	AX478005	AX478005 Sequence
	100	40.6	4.6	518	8	TAE577367	AJ577367 Triticum
	101	40.6	4.6	525	8	AB106111	AB106111 Populus n
	102	40.6	4.6	525	8	AB109804	AB109804 Populus n
	103	40.6	4.6	525	8	AB110613	AB110613 Populus n
	104	40.6	4.6	525	8	AB161108	AB161108 Populus n
	105	40.6	4.6	525	8	AB161109	AB161109 Populus n
	106	40.6	4.6	525	8	AB161112	AB161112 Malus x d
	107	40.6	4.6	670	8	AY515152	AY515152 Populus d
	108	40.6	4.6	1077	6	AX658815	AX658815 Sequence
	109	40.6	4.6	1077	6	AX658827	AX658827 Sequence
	110	40.6	4.6	2000	6	AX655393	AX655393 Sequence
c	111	40.6	4.6	11767	1	AE004536	AE004536 Pseudomon
	112	40	4.5	400	6	CQ663445	CQ663445 Sequence
	113	40	4.5	1432	6	CQ725969	CQ725969 Sequence
c	114	40	4.5	89201	9	AC093162	AC093162 Homo sapi
	115	39.8	4.5	745	8	AB027456	AB027456 Citrus un
	116	39.8	4.5	784	4	AY094175	AY094175 Oryctolag
	117	39.8	4.5	212221	2	AC136126	AC136126 Rattus no
c	118	39.8	4.5	220742	2	AC105644	AC105644 Rattus no
c	119	39.8	4.5	221323	2	AC106938	AC106938 Rattus no
	120	39.8	4.5	245853	2	AC125965	AC125965 Rattus no
	121	39.6	4.4	528	6	AX507940	AX507940 Sequence
	122	39.6	4.4	528	8	AF152907	AF152907 Arabidops
	123	39.6	4.4	799	8	AB027506	AB027506 Arabidops
	124	39.4	4.4	1242	10	AF307146	AF307146 Mus muscu
	125	39.4	4.4	1444	9	MFPBP	X73137 M.fascicula
c	126	39.4	4.4	88121	9	AC097226	AC097226 Papio anu
c	127	39.4	4.4	173505	2	AC141297	AC141297 Homo sapi
c	128	39.2	4.4	59124	2	AC106003	AC106003 Homo sapi
	129	39	4.4	974	6	CQ585477	CQ585477 Sequence
	130	39	4.4	1048	3	AY069195	AY069195 Drosophil
	131	39	4.4	2621	6	CQ611093	CQ611093 Sequence
	132	39	4.4	2974	6	CQ585476	CQ585476 Sequence
c	133	39	4.4	63551	2	AC012978	AC012978 Drosophil
	134	39	4.4	136933	3	AC005891	AC005891 Drosophil
	135	39	4.4	167544	3	AC093095	AC093095 Drosophil
	136	39	4.4	186444	3	AC093439	AC093439 Drosophil
	137	39	4.4	222787	3	AE003637	AE003637 Drosophil
	138	38.6	4.3	202442	2	AC110203	AC110203 Mus muscu
	139	38.4	4.3	522	8	AB181241	AB181241 Populus n
	140	38.4	4.3	164485	2	AC026106	AC026106 Homo sapi
c	141	38.4	4.3	186583	10	AC107669	AC107669 Mus muscu
c	142	38.4	4.3	207482	2	AC104402	AC104402 Rattus no
	143	38.4	4.3	210694	10	AC092095	AC092095 Mus muscu
	144	38.4	4.3	234391	2	AC121433	AC121433 Rattus no
c	145	38.4	4.3	300395	1	AE016785	AE016785 Pseudomon
	146	38	4.3	528	6	E38986	E38986 Method for
	147	37.8	4.2	492	6	CQ854990	CQ854990 Sequence
	148	37.8	4.2	492	6	AX477991	AX477991 Sequence
c	149	37.8	4.2	505	6	AR424142	AR424142 Sequence
c	150	37.8	4.2	505	6	AX984836	AX984836 Sequence
c	151	37.8	4.2	505	6	BD119695	BD119695 EST and e
	152	37.8	4.2	825	3	AK174865	AK174865 Ciona int
	153	37.8	4.2	866	8	AB062676	AB062676 Oryza sat
c	154	37.8	4.2	126847	9	AL445231	AL445231 Human DNA
	155	37.8	4.2	173224	2	AC116813	AC116813 Mus muscu
	156	37.8	4.2	181091	2	AC079373	AC079373 Mus muscu
c	157	37.8	4.2	198481	10	AL845486	AL845486 Mouse DNA
	158	37.6	4.2	2441	9	HSTBX5	Y09445 H.sapiens m
c	159	37.6	4.2	181617	2	AC119371	AC119371 Rattus no
	160	37.6	4.2	227298	10	AC106606	AC106606 Rattus no
	161	37.4	4.2	192554	2	AC121283	AC121283 Mus muscu
	162	37.2	4.2	687	6	CQ583599	CQ583599 Sequence
	163	37.2	4.2	2744	6	CQ583598	CQ583598 Sequence
	164	37.2	4.2	30334	2	AC013131	AC013131 Drosophil
	165	37.2	4.2	84055	3	AC004439	AC004439 Drosophil
	166	37.2	4.2	170868	3	AC092221	AC092221 Drosophil
c	167	37.2	4.2	197132	2	AC144519	AC144519 Mus muscu
	168	37.2	4.2	306696	3	AE003586	AE003586 Drosophil
c	169	37	4.2	142854	9	AC129918	AC129918 Homo sapi
c	170	37	4.2	167676	2	AC113153	AC113153 Homo sapi
	171	37	4.2	184788	2	AC147647	AC147647 Homo sapi
	172	36.8	4.1	528	6	E38985	E38985 Method for
	173	36.8	4.1	559	8	AY133813	AY133813 Arabidops
	174	36.8	4.1	564	10	AF300422	AF300422 Mus muscu
	175	36.8	4.1	780	8	AB027505	AB027505 Arabidops
	176	36.8	4.1	840	8	AY065378	AY065378 Arabidops
	177	36.8	4.1	855	6	AR148906	AR148906 Sequence
	178	36.8	4.1	855	6	BD206240	BD206240 Flowering
c	179	36.8	4.1	856	6	AR148907	AR148907 Sequence
c	180	36.8	4.1	856	6	BD206241	BD206241 Flowering
	181	36.8	4.1	856	6	AR491454	AR491454 Sequence
c	182	36.8	4.1	856	6	AR491455	AR491455 Sequence
	183	36.8	4.1	864	8	AB027504	AB027504 Arabidops
	184	36.8	4.1	1180	10	MMU43206	U43206 Mus musculu
	185	36.8	4.1	1202	10	AB046417	AB046417 Mus muscu
	186	36.8	4.1	1210	6	BD161812	BD161812 Method fo
	187	36.8	4.1	1217	10	BC083063	BC083063 Mus muscu
	188	36.8	4.1	1228	10	BC008169	BC008169 Mus muscu
	189	36.8	4.1	40536	2	AC110593	AC110593 Homo sapi
	190	36.8	4.1	41755	3	AF016423	AF016423 Caenorhab
	191	36.8	4.1	63747	2	AC127523	AC127523 Homo sapi
c	192	36.8	4.1	119420	2	AC109568	AC109568 Rattus no
	193	36.8	4.1	134095	2	AC006915	AC006915 Caenorhab
c	194	36.8	4.1	157236	2	AC149858	AC149858 Papio anu
c	195	36.8	4.1	166914	9	AC127522	AC127522 Homo sapi
c	196	36.8	4.1	194973	9	AC024474	AC024474 Homo sapi
	197	36.8	4.1	220215	2	AC135861	AC135861 Mus muscu
	198	36.8	4.1	223428	2	AC095912	AC095912 Rattus no
c	199	36.8	4.1	242449	10	AC102618	AC102618 Mus muscu
c	200	36.8	4.1	253026	2	AC098084	AC098084 Rattus no
c	201	36.8	4.1	346274	1	BX640443	BX640443 Bordetell
c	202	36.8	4.1	348014	1	BX640430	BX640430 Bordetell
	203	36.8	4.1	349672	1	BX640419	BX640419 Bordetell
	204	36.6	4.1	59605	2	AC103926	AC103926 Mus muscu
	205	36.6	4.1	124821	9	AC004983	AC004983 Homo sapi
c	206	36.6	4.1	190017	2	AC107782	AC107782 Mus muscu
c	207	36.6	4.1	339650	1	AP003583	AP003583 Nostoc sp
	208	36.4	4.1	1004	6	CQ855048	CQ855048 Sequence
	209	36.4	4.1	1004	6	AX478049	AX478049 Sequence
	210	36.4	4.1	2978	8	AK068736	AK068736 Oryza sat
c	211	36.4	4.1	10886	1	AE005847	AE005847 Caulobact
	212	36.4	4.1	110000	2	BX255276_11	Continuation (12 o
c	213	36.4	4.1	142350	5	BX664625	BX664625 Zebrafish
	214	36.4	4.1	196005	2	AC148865	AC148865 Canis fam
	215	36.2	4.1	1260	5	BX933665	BX933665 Gallus ga
c	216	36.2	4.1	24629	3	CER07D5	Z70685 Caenorhabdi
c	217	36.2	4.1	70388	2	AC068567	AC068567 Homo sapi
	218	36.2	4.1	151559	2	AC015863	AC015863 Homo sapi
	219	36.2	4.1	155204	8	AP003628	AP003628 Oryza sat
c	220	36.2	4.1	170761	9	CNS05TER	AL359240 Human chr
	221	36.2	4.1	179613	2	AC119216	AC119216 Mus muscu
	222	36.2	4.1	189448	2	AC103625	AC103625 Mus muscu
c	223	36.2	4.1	202842	10	AL607108	AL607108 Mouse DNA
	224	36.2	4.1	215238	10	AC122820	AC122820 Mus muscu
	225	36.2	4.1	227008	2	AP001771	AP001771 Homo sapi
	226	36	4.0	81082	10	AL844868	AL844868 Mouse DNA
c	227	36	4.0	98734	9	AC013277	AC013277 Homo sapi
c	228	36	4.0	138179	9	AC145217	AC145217 Homo sapi
	229	36	4.0	142085	9	AL359707	AL359707 Human DNA
	230	36	4.0	149635	9	CNS05TD7	AL356017 Human chr
	231	35.8	4.0	810	3	AY608669	AY608669 Branchios
c	232	35.8	4.0	121647	8	AC135565	AC135565 Medicago
c	233	35.8	4.0	153794	8	NC123A4	AL670009 Neurospor
c	234	35.8	4.0	186632	10	AC140047	AC140047 Mus muscu
	235	35.8	4.0	192520	2	AC129986	AC129986 Rattus no
	236	35.8	4.0	206979	10	AC112683	AC112683 Mus muscu
	237	35.6	4.0	687	3	DMU05243	U05243 Drosophila
	238	35.6	4.0	1351	5	BC082198	BC082198 Xenopus l

239	35.6	4.0	1364	10	BC030739	BC030739 Mus muscu
240	35.6	4.0	1406	10	BC002319	BC002319 Mus muscu
241	35.6	4.0	1651	10	BC052494	BC052494 Mus muscu
c 242	35.6	4.0	38102	9	AP001047	AP001047 Homo sapi
243	35.6	4.0	148463	2	AC012140	AC012140 Homo sapi
c 244	35.6	4.0	160456	9	BS000236	BS000236 Pan trogl
245	35.6	4.0	164380	9	AP001002	AP001002 Homo sapi
246	35.6	4.0	179556	2	AC018734	AC018734 Homo sapi
247	35.6	4.0	200317	9	HS69B13	AL035698 Human DNA
c 248	35.6	4.0	210567	2	AC074215	AC074215 Homo sapi
c 249	35.6	4.0	213466	2	AC019224	AC019224 Homo sapi
c 250	35.6	4.0	340000	9	AP001751	AP001751 Homo sapi
251	35.4	4.0	188624	10	AL772282	AL772282 Mouse DNA
252	35.4	4.0	200898	2	AC091695	AC091695 Bos tauru
253	35.2	4.0	786	8	AK107056	AK107056 Oryza sat
254	35.2	4.0	1226	6	CQ855018	CQ855018 Sequence
255	35.2	4.0	1226	6	AX478019	AX478019 Sequence
c 256	35.2	4.0	2000	6	AX655393	AX655393 Sequence
c 257	35.2	4.0	5032	8	AK067306	AK067306 Oryza sat
c 258	35.2	4.0	141899	9	AC006334	AC006334 Homo sapi
c 259	35.2	4.0	155704	9	AC073330	AC073330 Homo sapi
c 260	35.2	4.0	186596	2	AC141432	AC141432 Homo sapi
c 261	35.2	4.0	217068	2	AC079434	AC079434 Mus muscu
c 262	35.2	4.0	234429	9	AF311103	AF311103 Homo sapi
263	35.2	4.0	251364	10	MMAE000664	AE000664 Mus muscu
264	35.2	4.0	261600	10	AC125228	AC125228 Mus muscu
265	35	3.9	5190	6	CQ584432	CQ584432 Sequence
c 266	35	3.9	7218	6	I66494	I66494 Sequence 14
267	35	3.9	56575	9	AL355142	AL355142 Human DNA
c 268	35	3.9	94000	9	AP000562	AP000562 Homo sapi
c 269	35	3.9	110000	1	AE016822_04	Continuation (5 of
c 270	35	3.9	136490	8	CNS08CCE	AL929350 Oryza sat
271	35	3.9	151878	8	CNS08CD0	AL954632 Oryza sat
c 272	35	3.9	154492	2	AC137782	AC137782 Homo sapi
c 273	35	3.9	176757	4	AC095025	AC095025 Sus scrof
274	35	3.9	195405	10	AC132287	AC132287 Mus muscu
c 275	35	3.9	303450	1	SCO939130	AL939130 Streptomy
276	34.8	3.9	1383	6	AX934689	AX934689 Sequence
c 277	34.8	3.9	1918	3	AY122628	AY122628 Trypanopl
c 278	34.8	3.9	1918	3	AY122629	AY122629 Cryptobia
279	34.8	3.9	22979	9	AC009714	AC009714 Homo sapi
c 280	34.8	3.9	110000	2	AC073157_0	AC073157 Homo sapi
c 281	34.8	3.9	161148	4	AC127464	AC127464 Ornithorh
282	34.8	3.9	168666	2	AC131085	AC131085 Mus muscu
c 283	34.8	3.9	179087	5	BX072561	BX072561 Zebrafish
284	34.8	3.9	183586	9	AC092562	AC092562 Papio ham
c 285	34.8	3.9	184788	2	AC147647	AC147647 Homo sapi
286	34.8	3.9	189533	9	AC025678	AC025678 Homo sapi
c 287	34.8	3.9	198901	10	AC122248	AC122248 Mus muscu
288	34.8	3.9	204697	2	AC120995	AC120995 Rattus no
289	34.8	3.9	218222	10	AC127414	AC127414 Mus muscu
290	34.8	3.9	223714	2	AC109578	AC109578 Rattus no
c 291	34.8	3.9	236070	2	AC112571	AC112571 Rattus no
c 292	34.8	3.9	339940	2	AC139464	AC139464 Homo sapi
293	34.6	3.9	781	5	BX933434	BX933434 Gallus ga
294	34.6	3.9	1059	5	BX934603	BX934603 Gallus ga
295	34.6	3.9	1207	10	AF307147	AF307147 Mus muscu
296	34.6	3.9	6683	14	CDVREP	Y09629 Canine dist
297	34.6	3.9	15690	6	AX453975	AX453975 Sequence
298	34.6	3.9	15690	6	AX453976	AX453976 Sequence
299	34.6	3.9	15690	14	AF014953	AF014953 Canine di
300	34.6	3.9	15690	14	AF305419	AF305419 Canine di
301	34.6	3.9	15690	14	AF378705	AF378705 Canine di
302	34.6	3.9	18826	6	AX453977	AX453977 Sequence
303	34.6	3.9	42160	3	AC005804	AC005804 Leishmani
304	34.6	3.9	86958	9	AC004464	AC004464 Homo sapi
305	34.6	3.9	108797	3	AC121231	AC121231 Leishmani
306	34.6	3.9	155060	2	AC140158	AC140158 Felis cat
307	34.6	3.9	156383	2	AC135221	AC135221 Felis cat
c 308	34.6	3.9	160100	10	AL606988	AL606988 Mouse DNA
309	34.6	3.9	164180	9	AC016725	AC016725 Homo sapi
310	34.6	3.9	191358	10	AC068608	AC068608 Mus muscu
311	34.6	3.9	192181	9	AC133644	AC133644 Homo sapi
312	34.6	3.9	193944	4	AC147679	AC147679 Canis Fam
313	34.6	3.9	204006	2	AC134881	AC134881 Homo sapi
314	34.6	3.9	210775	2	AL732518	AL732518 Mus muscu
315	34.6	3.9	211544	9	AC025165	AC025165 Homo sapi
316	34.6	3.9	222817	2	AC137185	AC137185 Rattus no
317	34.6	3.9	225253	2	AC136482	AC136482 Rattus no
c 318	34.6	3.9	244170	2	AC130152	AC130152 Rattus no
c 319	34.6	3.9	249274	2	AC123229	AC123229 Rattus no
c 320	34.6	3.9	256034	2	AC095559	AC095559 Rattus no
c 321	34.6	3.9	257310	1	AE017320	AE017320 Desulfovi
c 322	34.6	3.9	309805	2	AC026340	AC026340 Homo sapi
c 323	34.6	3.9	348068	1	BX572604	BX572604 Rhodopseu
324	34.4	3.9	613	6	CQ855042	CQ855042 Sequence
325	34.4	3.9	613	6	AX478043	AX478043 Sequence
c 326	34.4	3.9	67972	2	AC100719	AC100719 Mus muscu
c 327	34.4	3.9	142201	9	AC124248	AC124248 Homo sapi
c 328	34.4	3.9	157101	2	AC145541	AC145541 Oryctolag
329	34.4	3.9	159397	9	AC068544	AC068544 Homo sapi
c 330	34.4	3.9	171206	2	AC026573	AC026573 Homo sapi
331	34.4	3.9	172015	2	AC149194	AC149194 Papio anu
332	34.4	3.9	177010	2	AC140372	AC140372 Mus muscu
333	34.4	3.9	182010	2	AC110270	AC110270 Mus muscu
334	34.4	3.9	198303	2	AC117592	AC117592 Mus muscu
335	34.4	3.9	198471	2	AC108424	AC108424 Mus muscu
336	34.4	3.9	214111	10	AC123694	AC123694 Mus muscu
337	34.4	3.9	231008	2	AC129166	AC129166 Rattus no
c 338	34.4	3.9	231499	2	AC111629	AC111629 Rattus no
c 339	34.4	3.9	239352	2	AC106294	AC106294 Rattus no
c 340	34.4	3.9	241803	2	AC096458	AC096458 Rattus no
341	34.4	3.9	246444	2	AC130772	AC130772 Rattus no
c 342	34.4	3.9	257887	2	AC092193	AC092193 Bos tauru
343	34.4	3.9	265074	2	AC103024	AC103024 Rattus no
c 344	34.4	3.9	273285	1	AE017304	AE017304 Thermus t
345	34.4	3.9	290285	2	AC116074	AC116074 Rattus no
c 346	34.2	3.8	413	6	AX658802	AX658802 Sequence
347	34.2	3.8	555	6	AX658864	AX658864 Sequence
348	34.2	3.8	850	6	CQ855024	CQ855024 Sequence
349	34.2	3.8	850	6	AX478025	AX478025 Sequence
350	34.2	3.8	1724	8	AK107655	AK107655 Oryza sat
351	34.2	3.8	2649	10	BC006600	BC006600 Mus muscu
352	34.2	3.8	6045	1	AF361867	AF361867 Azospiril
353	34.2	3.8	107914	2	AP003949	AP003949 Oryza sat
c 354	34.2	3.8	110000	2	AL732359_07	Continuation (8 of
c 355	34.2	3.8	110000	2	BX255276_10	Continuation (11 o
c 356	34.2	3.8	142832	8	AP003620	AP003620 Oryza sat
357	34.2	3.8	149430	14	AY464052	AY464052 Equine he
358	34.2	3.8	150224	14	AY665713	AY665713 Equine he
c 359	34.2	3.8	172200	2	AC148623	AC148623 Otolemur
c 360	34.2	3.8	180555	9	AC079384	AC079384 Homo sapi
c 361	34.2	3.8	183894	9	AC040970	AC040970 Homo sapi
362	34.2	3.8	193113	5	AL935197	AL935197 Zebrafish
363	34.2	3.8	210933	2	AC027394	AC027394 Homo sapi
c 364	34.2	3.8	225879	10	AL603787	AL603787 Mouse DNA
365	34.2	3.8	241795	2	AC123410	AC123410 Rattus no
366	34.2	3.8	349737	1	BX572597	BX572597 Rhodopseu
367	34	3.8	325	8	AJ837301	AJ837301 Arabidops
368	34	3.8	1667	8	AF322083	AF322083 Microbotr
c 369	34	3.8	13606	6	AX251316	AX251316 Sequence
c 370	34	3.8	13606	6	AX278003	AX278003 Sequence
c 371	34	3.8	13606	6	AX323700	AX323700 Sequence
c 372	34	3.8	13606	6	AX346713	AX346713 Sequence
c 373	34	3.8	110000	2	LMFLCHR36_07	Continuation (8 of
374	34	3.8	125508	9	AC006345	AC006345 Homo sapi
375	34	3.8	153099	2	AC149983	AC149983 Strongylo
c 376	34	3.8	153350	8	CNS08C9T	AL772415 Oryza sat
377	34	3.8	164190	10	AC121874	AC121874 Mus muscu
378	34	3.8	165423	9	CNS07ECV	AL442663 Human chr
379	34	3.8	194774	2	AC127648	AC127648 Rattus no
380	34	3.8	196011	2	AC113893	AC113893 Rattus no
c 381	34	3.8	207701	2	BX545856	BX545856 Danio rer
382	34	3.8	230232	2	AC104292	AC104292 Rattus no
c 383	34	3.8	240321	10	AC138329	AC138329 Mus muscu
c 384	34	3.8	250424	2	AC129341	AC129341 Rattus no

	385	34	3.8	251914	2	AC111366 AC111366 Rattus no
c	386	34	3.8	282933	2	AC122970 AC122970 Rattus no
	387	34	3.8	303720	2	AC126863 AC126863 Rattus no
c	388	34	3.8	304399	2	AC129354 AC129354 Rattus no
	389	33.8	3.8	730	6	CQ832296 CQ832296 Sequence
	390	33.8	3.8	801	1	AY452767 AY452767 Chlorobiu
	391	33.8	3.8	991	8	AK108673 AK108673 Oryza sat
	392	33.8	3.8	1083	6	CQ610875 CQ610875 Sequence
	393	33.8	3.8	1246	3	AY089645 AY089645 Drosophil
	394	33.8	3.8	2959	8	AK100491 AK100491 Oryza sat
	395	33.8	3.8	3144	6	CQ610874 CQ610874 Sequence
	396	33.8	3.8	5436	6	CQ610871 CQ610871 Sequence
c	397	33.8	3.8	31557	3	AC004267 AC004267 Drosophil
	398	33.8	3.8	58041	10	BX510318 BX510318 Mouse DNA
c	399	33.8	3.8	64786	2	AC017805 AC017805 Drosophil
c	400	33.8	3.8	125291	9	AP000646 AP000646 Homo sapi
	401	33.8	3.8	150202	5	AL929343 AL929343 Zebrafish
c	402	33.8	3.8	171832	9	AC079942 AC079942 Homo sapi
c	403	33.8	3.8	172239	2	AC069587 AC069587 Homo sapi
	404	33.8	3.8	173845	9	AC018662 AC018662 Human Chr
c	405	33.8	3.8	181518	2	AC141952 AC141952 Rattus no
	406	33.8	3.8	182897	3	AC092232 AC092232 Drosophil
	407	33.8	3.8	183082	2	AC141330 AC141330 Rattus no
	408	33.8	3.8	183416	10	AL671269 AL671269 Mouse DNA
c	409	33.8	3.8	189844	5	BX649492 BX649492 Zebrafish
c	410	33.8	3.8	196392	2	AC120322 AC120322 Rattus no
	411	33.8	3.8	196904	10	AC126447 AC126447 Mus muscu
c	412	33.8	3.8	205825	2	AP000881 AP000881 Homo sapi
c	413	33.8	3.8	207639	10	AL844581 AL844581 Mouse DNA
	414	33.8	3.8	214042	10	AC127556 AC127556 Mus muscu
c	415	33.8	3.8	220303	2	AC111672 AC111672 Rattus no
	416	33.8	3.8	227946	10	AC124175 AC124175 Mus muscu
c	417	33.8	3.8	241280	2	AC115158 AC115158 Rattus no
	418	33.8	3.8	246443	2	AC112892 AC112892 Rattus no
	419	33.8	3.8	250714	2	AC094792 AC094792 Rattus no
	420	33.8	3.8	259160	2	AC114105 AC114105 Rattus no
c	421	33.8	3.8	268261	2	AC112896 AC112896 Rattus no
c	422	33.8	3.8	289893	3	AE003576 AE003576 Drosophil
	423	33.8	3.8	344615	1	BX569695 BX569695 Synechoco
c	424	33.8	3.8	347625	1	BX248356 BX248356 Corynebac
	425	33.8	3.8	349116	1	AP003003 AP003003 Mesorhizo
	426	33.6	3.8	213	1	AF059494 AF059494 Aeromonas
c	427	33.6	3.8	1254	9	BT006704 BT006704 Homo sapi
c	428	33.6	3.8	1254	9	CR457033 CR457033 Homo sapi
c	429	33.6	3.8	1254	12	BT007999 BT007999 Synthetic
	430	33.6	3.8	1260	10	RATGP330 M31051 Rat Heymann
	431	33.6	3.8	1373	10	BC082020 BC082020 Rattus no
	432	33.6	3.8	1427	5	LPAY18674 Y18674 Lipophrys p
c	433	33.6	3.8	1442	9	BC003573 BC003573 Homo sapi
c	434	33.6	3.8	1606	6	AR430603 AR430603 Sequence
	435	33.6	3.8	1644	10	RN45KDB Z11995 R.norvegicu
c	436	33.6	3.8	2097	6	AR454557 AR454557 Sequence
c	437	33.6	3.8	2097	6	AX281763 AX281763 Sequence
	438	33.6	3.8	2124	10	BC079400 BC079400 Rattus no
	439	33.6	3.8	2768	10	RN45KDA Z11994 R.norvegicu
c	440	33.6	3.8	2884	6	AX835108 AX835108 Sequence
c	441	33.6	3.8	2884	9	AK097933 AK097933 Homo sapi
	442	33.6	3.8	23373	9	AC133009 AC133009 Homo sapi
c	443	33.6	3.8	50121	9	AL354700 AL354700 Human DNA
	444	33.6	3.8	57348	2	AC101362 AC101362 Mus muscu
	445	33.6	3.8	110000	1	AE017282_26 Continuation (27 o
	446	33.6	3.8	110000	1	AE017282_27 Continuation (28 o
	447	33.6	3.8	110000	2	AC106831_1 Continuation (2 of
c	448	33.6	3.8	110000	10	AF162137_0 AF162137 Mus muscu
c	449	33.6	3.8	110000	10	AF162137_1 Continuation (2 of
c	450	33.6	3.8	124551	2	AC005809 AC005809 Homo sapi
	451	33.6	3.8	135351	9	AC068279 AC068279 Homo sapi
c	452	33.6	3.8	135991	2	AC148750 AC148750 Dasypus n
c	453	33.6	3.8	136148	2	AC150730 AC150730 Atelerix
c	454	33.6	3.8	137691	9	AC123789 AC123789 Homo sapi
c	455	33.6	3.8	148772	2	AC055826 AC055826 Homo sapi
c	456	33.6	3.8	152336	2	AC009594 AC009594 Homo sapi
c	457	33.6	3.8	155818	9	AL954253 AL954253 Pan trogl
c	458	33.6	3.8	161533	9	AC093001 AC093001 Homo sapi
	459	33.6	3.8	163332	2	AC072027 AC072027 Homo sapi
	460	33.6	3.8	164383	2	AC068023 AC068023 Homo sapi
	461	33.6	3.8	168058	2	AC141611 AC141611 Homo sapi
c	462	33.6	3.8	170088	2	AC025119 AC025119 Homo sapi
c	463	33.6	3.8	170569	2	AC102865 AC102865 Mus muscu
	464	33.6	3.8	172772	10	AC121923 AC121923 Mus muscu
c	465	33.6	3.8	174578	9	AC013287 AC013287 Homo sapi
	466	33.6	3.8	176719	2	AC140858 AC140858 Homo sapi
c	467	33.6	3.8	182012	9	AL359846 AL359846 Human DNA
	468	33.6	3.8	195169	9	AC017109 AC017109 Homo sapi
c	469	33.6	3.8	204710	2	AC148852 AC148852 Otolemur
c	470	33.6	3.8	221255	10	AL671536 AL671536 Mouse DNA
c	471	33.6	3.8	254830	2	AC095718 AC095718 Rattus no
	472	33.6	3.8	281728	2	AC126684 AC126684 Mus muscu
c	473	33.4	3.8	678	6	AX934094 AX934094 Sequence
c	474	33.4	3.8	678	6	AX934096 AX934096 Sequence
	475	33.4	3.8	843	8	AY148490 AY148490 Triticum
	476	33.4	3.8	934	8	TA3LEA X56882 Wheat mRNA
	477	33.4	3.8	1191	8	BLYPDIC L33252 Hordeum vul
	478	33.4	3.8	1772	8	BLYPDIB L33251 Hordeum vul
	479	33.4	3.8	1816	8	BLYPDIA L33250 Hordeum vul
	480	33.4	3.8	2370	10	MMFBLN2S02 AF135239 Mus muscu
	481	33.4	3.8	3969	10	BC005443 BC005443 Mus muscu
	482	33.4	3.8	4377	10	MMRFIB2 X75285 M.musculus
c	483	33.4	3.8	8297	1	ECDAMOPRA Z19601 E.coli dam
	484	33.4	3.8	10905	1	AE015348 AE015348 Shigella
c	485	33.4	3.8	18887	9	AC124974 AC124974 Homo sapi
c	486	33.4	3.8	35197	9	AC005782 AC005782 Homo sapi
	487	33.4	3.8	38253	9	AC093232 AC093232 Homo sapi
c	488	33.4	3.8	58318	10	AL645748 AL645748 Mouse DNA
c	489	33.4	3.8	63965	2	AC100562 AC100562 Mus muscu
c	490	33.4	3.8	68048	9	AC004764 AC004764 Homo sapi
	491	33.4	3.8	101990	10	AL929248 AL929248 Mouse DNA
	492	33.4	3.8	110000	1	U00096_35 Continuation (36 o
	493	33.4	3.8	110000	1	ECOUW67_2 Continuation (3 of
	494	33.4	3.8	113428	9	CR626893 CR626893 Human DNA
c	495	33.4	3.8	122867	9	CR626925 CR626925 Human DNA
	496	33.4	3.8	131906	2	AC083983 AC083983 Homo sapi
	497	33.4	3.8	140386	9	AC015921 AC015921 Homo sapi
c	498	33.4	3.8	141833	9	AL442063 AL442063 Human DNA
	499	33.4	3.8	147585	8	AP004745 AP004745 Oryza sat
	500	33.4	3.8	154508	2	AC083974 AC083974 Homo sapi
	501	33.4	3.8	158857	8	AP005470 AP005470 Oryza sat
	502	33.4	3.8	165904	2	AL158148 AL158148 Homo sapi
c	503	33.4	3.8	169138	2	AC150989 AC150989 Bos tauru
c	504	33.4	3.8	174513	9	AC104308 AC104308 Homo sapi
	505	33.4	3.8	175354	2	AC121990 AC121990 Mus muscu
c	506	33.4	3.8	175445	2	AC115501 AC115501 Rattus no
c	507	33.4	3.8	178030	9	AC008406 AC008406 Homo sapi
c	508	33.4	3.8	189050	2	AC142566 AC142566 Bos tauru
c	509	33.4	3.8	196988	9	AP002761 AP002761 Homo sapi
	510	33.4	3.8	198958	9	AC020688 AC020688 Homo sapi
	511	33.4	3.8	202109	2	AC099707 AC099707 Mus muscu
	512	33.4	3.8	204340	2	AC019238 AC019238 Homo sapi
c	513	33.4	3.8	208239	2	AC021988 AC021988 Homo sapi
c	514	33.4	3.8	210145	10	AC131764 AC131764 Mus muscu
c	515	33.4	3.8	216481	2	AC125380 AC125380 Mus muscu
c	516	33.4	3.8	217817	2	AC145402 AC145402 Gorilla g
c	517	33.4	3.8	227430	2	AC091590 AC091590 Homo sapi
	518	33.4	3.8	233212	10	AL845161 AL845161 Mouse DNA
c	519	33.4	3.8	238252	2	AC095633 AC095633 Rattus no
	520	33.4	3.8	240364	2	AC150677 AC150677 Bos tauru
c	521	33.4	3.8	245117	2	AC111284 AC111284 Rattus no
	522	33.4	3.8	250884	2	AC123281 AC123281 Rattus no
c	523	33.4	3.8	289816	1	AE016992 AE016992 Shigella
	524	33.4	3.8	301660	1	AE016768 AE016768 Escherich
	525	33.4	3.8	340857	1	AP003010 AP003010 Mesorhizo
	526	33.2	3.7	644	6	CQ721388 CQ721388 Sequence
	527	33.2	3.7	691	9	S46843S2 S46845 2',3'-cycli
	528	33.2	3.7	691	9	S50013S2 S50014 2',3'-cycli
	529	33.2	3.7	785	9	HSA333060 AJ333060 Homo sapi
	530	33.2	3.7	852	6	BD181871 BD181871 Alveolar

	531	33.2	3.7	852	6	I08580 Sequence 26
	532	33.2	3.7	852	6	I09317 Sequence 8
c	533	33.2	3.7	854	6	BD186586 Nucleic a
c	534	33.2	3.7	854	6	BD018096 Novel gen
c	535	33.2	3.7	854	6	BD098034 Novel gen
	536	33.2	3.7	858	6	I08709 Sequence 5
	537	33.2	3.7	858	6	I08779 Sequence 4
	538	33.2	3.7	859	9	HUMSPLA J03517 Human pulmo
	539	33.2	3.7	861	6	BD181870 Alveolar
	540	33.2	3.7	861	6	I08033 Sequence 7
	541	33.2	3.7	861	6	I08579 Sequence 24
	542	33.2	3.7	861	6	I09316 Sequence 6
	543	33.2	3.7	876	9	BC005913 Homo sapi
	544	33.2	3.7	899	6	CQ855000 Sequence
	545	33.2	3.7	899	6	AX478001 Sequence
	546	33.2	3.7	991	9	HUMSP5 J03553 Human pulmo
	547	33.2	3.7	997	10	AF295405 AF295405 Rattus no
	548	33.2	3.7	1266	12	AY335577 AY335577 Synthetic
	549	33.2	3.7	1493	9	BC066949 BC066949 Homo sapi
	550	33.2	3.7	1496	9	AK058094 AK058094 Homo sapi
	551	33.2	3.7	1633	4	BOVCNPASE M27606 Bovine 2',3
	552	33.2	3.7	1641	6	BD186346 BD186346 STAT6 act
	553	33.2	3.7	1643	4	BTCNPASE Y00405 Bos taurus
	554	33.2	3.7	1689	9	AB051117 AB051117 Macaca fa
	555	33.2	3.7	1762	6	BD186290 BD186290 STAT6 act
	556	33.2	3.7	1762	9	HUMCNPDEA M19650 Human 2',3'
	557	33.2	3.7	1928	10	BC016662 BC016662 Mus muscu
	558	33.2	3.7	2285	4	BOVCNP J02659 Bovine 2',3
	559	33.2	3.7	2598	9	BC011046 BC011046 Homo sapi
	560	33.2	3.7	2608	9	AK098384 AK098384 Homo sapi
	561	33.2	3.7	2609	9	D13144S1 D13144 Homo sapien
	562	33.2	3.7	2612	9	BC001362 BC001362 Homo sapi
	563	33.2	3.7	2634	9	AK026876 AK026876 Homo sapi
	564	33.2	3.7	2644	9	BC006392 BC006392 Homo sapi
	565	33.2	3.7	2725	9	BC028040 BC028040 Homo sapi
	566	33.2	3.7	2820	5	BC057749 BC057749 Xenopus l
	567	33.2	3.7	3489	10	AF041822 AF041822 Mus muscu
	568	33.2	3.7	3667	10	BC049119 BC049119 Mus muscu
c	569	33.2	3.7	9343	14	HCV1480 Y13184 Hepatitis C
	570	33.2	3.7	10029	1	AE014591 AE014591 Brucella
c	571	33.2	3.7	10241	1	AE009670 AE009670 Brucella
	572	33.2	3.7	15529	10	CR536618 CR536618 Mouse DNA
	573	33.2	3.7	20461	1	AF375657 AF375657 Aeromonas
	574	33.2	3.7	20838	8	AP006399 AP006399 Lotus cor
	575	33.2	3.7	65870	2	AC132912 AC132912 Homo sapi
	576	33.2	3.7	67911	10	AL603834 AL603834 Mouse DNA
	577	33.2	3.7	70185	2	AC138349 AC138349 Homo sapi
c	578	33.2	3.7	70462	2	AC129532 AC129532 Homo sapi
c	579	33.2	3.7	110000	2	AC129397_0 AC129397 Rattus no
c	580	33.2	3.7	110000	2	AC151852_0 AC151852 Takifugu
c	581	33.2	3.7	110000	2	LMPLCHR16_08 Continuation (9 of
c	582	33.2	3.7	114375	4	AB113357 AB113357 Sus scrof
c	583	33.2	3.7	126475	2	AC123787 AC123787 Homo sapi
c	584	33.2	3.7	126943	2	AC151712 AC151712 Mus muscu
c	585	33.2	3.7	134847	2	AC124061 AC124061 Homo sapi
c	586	33.2	3.7	138444	10	AC135116 AC135116 Mus muscu
c	587	33.2	3.7	141578	8	AC124141 AC124141 Oryza sat
c	588	33.2	3.7	145363	2	AC079213 AC079213 Homo sapi
c	589	33.2	3.7	146382	4	AB113356 AB113356 Sus scrof
c	590	33.2	3.7	147004	8	AP003291 AP003291 Oryza sat
c	591	33.2	3.7	153715	10	AC126681 AC126681 Mus muscu
	592	33.2	3.7	157226	9	AC018902 AC018902 Homo sapi
	593	33.2	3.7	159726	9	AC125257 AC125257 Homo sapi
	594	33.2	3.7	162777	2	AC124100 AC124100 Mus muscu
c	595	33.2	3.7	166572	2	AC091508 AC091508 Felis cat
c	596	33.2	3.7	168017	2	AC115017 AC115017 Mus muscu
c	597	33.2	3.7	170126	2	AC123770 AC123770 Homo sapi
c	598	33.2	3.7	171196	2	AP001369 AP001369 Homo sapi
c	599	33.2	3.7	171810	2	AC128062 AC128062 Rattus no
	600	33.2	3.7	184157	2	AC073438 AC073438 Homo sapi
	601	33.2	3.7	202357	5	AL831748 AL831748 Zebrafish
	602	33.2	3.7	203050	1	AL646071 AL646071 Ralstonia
	603	33.2	3.7	205033	2	AC111383 AC111383 Rattus no
	604	33.2	3.7	212177	10	AC115356 AC115356 Mus muscu
	605	33.2	3.7	219288	2	AC131321 AC131321 Mus muscu
	606	33.2	3.7	220714	2	BX936300 BX936300 Mus muscu
	607	33.2	3.7	222048	2	AC095529 AC095529 Rattus no
	608	33.2	3.7	234963	2	AC094843 AC094843 Rattus no
c	609	33.2	3.7	237332	2	AC131846 AC131846 Rattus no
c	610	33.2	3.7	240561	2	AC129456 AC129456 Rattus no
	611	33.2	3.7	242500	10	AC095787 AC095787 Rattus no
	612	33.2	3.7	257701	1	BX640422 BX640422 Bordetell
c	613	33.2	3.7	262597	2	AC094133 AC094133 Rattus no
	614	33.2	3.7	263257	2	AC125564 AC125564 Rattus no
	615	33.2	3.7	275598	2	AC021768 AC021768 Mus muscu
	616	33.2	3.7	301068	1	AE017231 AE017231 Mycobacte
c	617	33.2	3.7	340756	2	AC125366 AC125366 Rattus no
c	618	33.2	3.7	346287	1	BX640450 BX640450 Bordetell
	619	33.2	3.7	348878	2	AC130911 AC130911 Rattus no
c	620	33	3.7	231	11	G24497 G24497 human STS W
c	621	33	3.7	342	11	G25185 G25185 human STS E
	622	33	3.7	522	6	AX658850 AX658850 Sequence
	623	33	3.7	997	8	HVABAIP X13498 Barley pHVA
	624	33	3.7	1322	5	CR353195 CR353195 Gallus ga
	625	33	3.7	1350	8	AK110622 AK110622 Oryza sat
	626	33	3.7	1419	10	BC057979 BC057979 Mus muscu
	627	33	3.7	1451	10	BC032170 BC032170 Mus muscu
	628	33	3.7	1452	10	AJ639614 AJ639614 Mus muscu
	629	33	3.7	1478	10	S67967 S67967 heparin bin
	630	33	3.7	1585	6	E12643 E12643 cDNA encodi
	631	33	3.7	1804	8	HVHVA1 X78205 H.vulgare (
	632	33	3.7	2448	8	AF326116 AF326116 Agastache
	633	33	3.7	2619	5	S65205 S65205 endothelial
	634	33	3.7	2753	10	BC059887 BC059887 Mus muscu
	635	33	3.7	2902	6	CQ777321 CQ777321 Sequence
	636	33	3.7	2902	6	AX305444 AX305444 Sequence
	637	33	3.7	2902	10	MUSHBP44 D00622 Mus musculu
	638	33	3.7	2913	10	BC046641 BC046641 Mus muscu
	639	33	3.7	4118	6	CQ843129 CQ843129 Sequence
	640	33	3.7	4118	9	AK126097 AK126097 Homo sapi
	641	33	3.7	5390	5	CCQUEK1 X83288 C.coturnix
	642	33	3.7	77292	8	BX842596 BX842596 Neurospor
c	643	33	3.7	78520	9	AC004455 AC004455 Homo sapi
	644	33	3.7	86049	9	AL591742 AL591742 Human DNA
	645	33	3.7	86363	9	HSJ539E24 AL121920 Human DNA
	646	33	3.7	110000	1	BX571966_21 Continuation (22 o
c	647	33	3.7	154413	9	AC146043 AC146043 Pan trogl
c	648	33	3.7	162397	2	AC011098 AC011098 Homo sapi
	649	33	3.7	162871	10	AC132597 AC132597 Mus muscu
c	650	33	3.7	168814	10	AL591582 AL591582 Mouse DNA
c	651	33	3.7	169993	2	AC144884 AC144884 Papio anu
c	652	33	3.7	173294	2	AC105317 AC105317 Homo sapi
	653	33	3.7	175728	2	AC123394 AC123394 Rattus no
c	654	33	3.7	175728	2	AC123394 AC123394 Rattus no
	655	33	3.7	176550	2	AC147354 AC147354 Xenopus t
c	656	33	3.7	178292	2	AC120830 AC120830 Rattus no
c	657	33	3.7	182490	2	AC068572 AC068572 Homo sapi
c	658	33	3.7	183807	10	AC101956 AC101956 Mus muscu
	659	33	3.7	184451	9	AC016768 AC016768 Homo sapi
c	660	33	3.7	188038	2	AC151266 AC151266 Mus muscu
	661	33	3.7	189778	2	AC132897 AC132897 Mus muscu
	662	33	3.7	194995	9	AC018696 AC018696 Homo sapi
	663	33	3.7	200908	2	AC108985 AC108985 Rattus no
c	664	33	3.7	200908	2	AC108985 AC108985 Rattus no
	665	33	3.7	201220	2	AC146868 AC146868 Xenopus t
c	666	33	3.7	203345	10	AL606746 AL606746 Mouse DNA
c	667	33	3.7	209144	2	AC107731 AC107731 Mus muscu
c	668	33	3.7	213847	2	AC120262 AC120262 Rattus no
	669	33	3.7	214178	2	AC106259 AC106259 Rattus no
c	670	33	3.7	216031	9	AC011328 AC011328 Homo sapi
c	671	33	3.7	225678	2	AC126963 AC126963 Rattus no
	672	33	3.7	230957	2	AC121192 AC121192 Rattus no
	673	33	3.7	235420	2	AC105668 AC105668 Rattus no
c	674	33	3.7	237622	2	AC097299 AC097299 Rattus no
c	675	33	3.7	246719	2	AC115431 AC115431 Rattus no
c	676	33	3.7	248333	2	AC097969 AC097969 Rattus no

	677	33	3.7	252132	2	AC127903 AC127903 Rattus no
c	678	33	3.7	252132	2	AC127903 AC127903 Rattus no
	679	33	3.7	255476	2	AC113674 AC113674 Rattus no
	680	33	3.7	256873	2	AC125949 AC125949 Rattus no
c	681	33	3.7	259014	2	AC107273 AC107273 Rattus no
	682	33	3.7	261990	2	AC111513 AC111513 Rattus no
	683	33	3.7	272301	2	AC133673 AC133673 Rattus no
	684	33	3.7	295449	2	AC105819 AC105819 Rattus no
c	685	33	3.7	299800	1	AP005028 AP005028 Streptomy
	686	32.8	3.7	282	6	AR251413 AR251413 Sequence
c	687	32.8	3.7	542	11	G93535 G93535 S208P6363FF
	688	32.8	3.7	611	3	OVD1PROTN X87991 O.volvulus
c	689	32.8	3.7	781	6	CQ789640 CQ789640 Sequence
	690	32.8	3.7	822	3	ONGANTIG M27807 O.volvulus
	691	32.8	3.7	822	6	I11816 I11816 Sequence 1
	692	32.8	3.7	894	3	AB100032 AB100032 Echinococ
c	693	32.8	3.7	970	6	CQ789638 CQ789638 Sequence
c	694	32.8	3.7	1505	9	BC062459 BC062459 Homo sapi
	695	32.8	3.7	1667	8	AF322079 AF322079 Microbotr
	696	32.8	3.7	1667	8	AF322080 AF322080 Microbotr
	697	32.8	3.7	1667	8	AF322082 AF322082 Microbotr
	698	32.8	3.7	1668	8	AF322081 AF322081 Microbotr
c	699	32.8	3.7	2075	5	AJ720726 AJ720726 Gallus ga
c	700	32.8	3.7	2199	6	AX714618 AX714618 Sequence
c	701	32.8	3.7	2199	9	AK057097 AK057097 Homo sapi
	702	32.8	3.7	2849	10	RNO245619 AJ245619 Rattus no
c	703	32.8	3.7	3479	6	AR528514 AR528514 Sequence
c	704	32.8	3.7	3479	6	AX463990 AX463990 Sequence
c	705	32.8	3.7	3479	9	AY358358 AY358358 Homo sapi
	706	32.8	3.7	9905	6	AX379470 AX379470 Sequence
c	707	32.8	3.7	10561	6	CQ789655 CQ789655 Sequence
	708	32.8	3.7	10618	1	AE013539 AE013539 Methanosa
c	709	32.8	3.7	11006	6	CQ789654 CQ789654 Sequence
	710	32.8	3.7	46530	2	BX293554_5 Continuation (6 of
c	711	32.8	3.7	67645	9	AL356486 AL356486 Human DNA
c	712	32.8	3.7	72151	9	AC091890 AC091890 Homo sapi
	713	32.8	3.7	81763	9	AC107208 AC107208 Homo sapi
c	714	32.8	3.7	103034	2	AC067978 AC067978 Homo sapi
c	715	32.8	3.7	110000	2	AC095743_1 Continuation (2 of
	716	32.8	3.7	111934	9	AF281074 AF281074 Homo sapi
	717	32.8	3.7	116039	9	AC007362 AC007362 Homo sapi
c	718	32.8	3.7	123556	9	HS507I15 Z98950 Human DNA s
c	719	32.8	3.7	123925	9	AC003976 AC003976 Homo sapi
	720	32.8	3.7	130805	9	AC118283 AC118283 Homo sapi
	721	32.8	3.7	131537	2	AC148738 AC148738 Ornithorh
c	722	32.8	3.7	135240	9	AL136362 AL136362 Human DNA
c	723	32.8	3.7	136858	8	AC134345 AC134345 Oryza sat
	724	32.8	3.7	140553	8	AC091666 AC091666 Oryza sat
	725	32.8	3.7	143052	2	AC079207 AC079207 Homo sapi
	726	32.8	3.7	144324	9	AC097526 AC097526 Homo sapi
c	727	32.8	3.7	145952	2	AC135921 AC135921 Oryza sat
c	728	32.8	3.7	147352	8	AC137746 AC137746 Oryza sat
	729	32.8	3.7	151279	2	AC137648 AC137648 Bos tauru
	730	32.8	3.7	151972	8	AC131175 AC131175 Genomic s
c	731	32.8	3.7	153082	2	AC142533 AC142533 Homo sapi
c	732	32.8	3.7	154318	9	AC026791 AC026791 Homo sapi
	733	32.8	3.7	154828	9	AC069363 AC069363 Homo sapi
	734	32.8	3.7	156555	9	AC026756 AC026756 Homo sapi
c	735	32.8	3.7	156683	9	AC091891 AC091891 Homo sapi
	736	32.8	3.7	162657	9	BX649569 BX649569 Human DNA
	737	32.8	3.7	162685	2	AC110880 AC110880 Mus muscu
	738	32.8	3.7	170760	2	AC004071 AC004071 Homo sapi
c	739	32.8	3.7	174080	2	AF217246 AF217246 Homo sapi
c	740	32.8	3.7	174306	10	AC140444 AC140444 Mus muscu
	741	32.8	3.7	177393	2	AC079019 AC079019 Homo sapi
c	742	32.8	3.7	177522	9	AC093566 AC093566 Homo sapi
	743	32.8	3.7	177826	2	AC016852 AC016852 Homo sapi
c	744	32.8	3.7	179934	2	AC128793 AC128793 Rattus no
	745	32.8	3.7	179980	2	AC121271 AC121271 Mus muscu
c	746	32.8	3.7	181389	2	AC099496 AC099496 Homo sapi
	747	32.8	3.7	182747	9	AC090964 AC090964 Papio anu
c	748	32.8	3.7	183249	9	AC004828 AC004828 Homo sapi
c	749	32.8	3.7	186387	10	AC122885 AC122885 Mus muscu
c	750	32.8	3.7	187005	9	BX664735 BX664735 Human DNA
	751	32.8	3.7	188584	10	AC069563 AC069563 Mus muscu
c	752	32.8	3.7	191560	2	AC145530 AC145530 Callithri
	753	32.8	3.7	195423	2	AC087151 AC087151 Mus muscu
	754	32.8	3.7	196674	2	AC150894 AC150894 Mus muscu
	755	32.8	3.7	201178	10	AC098714 AC098714 Mus muscu
	756	32.8	3.7	205503	2	AC141489 AC141489 Rattus no
	757	32.8	3.7	208026	9	AP006292 AP006292 Homo sapi
	758	32.8	3.7	211156	2	AC136939 AC136939 Homo sapi
	759	32.8	3.7	217001	10	AC125052 AC125052 Mus muscu
	760	32.8	3.7	222994	2	AC094289 AC094289 Rattus no
	761	32.8	3.7	223581	2	AC144543 AC144543 Mus muscu
c	762	32.8	3.7	226758	2	AC121186 AC121186 Rattus no
c	763	32.8	3.7	233831	2	AC107338 AC107338 Rattus no
	764	32.8	3.7	238973	2	AC133265 AC133265 Rattus no
	765	32.8	3.7	241987	2	AC101725 AC101725 Mus muscu
c	766	32.8	3.7	244281	2	AC125891 AC125891 Rattus no
c	767	32.8	3.7	246238	2	AC120998 AC120998 Rattus no
c	768	32.8	3.7	252473	2	AC093972 AC093972 Rattus no
	769	32.8	3.7	268356	1	TACID5 AL445067 Thermopla
	770	32.8	3.7	270654	2	AC096084 AC096084 Rattus no
c	771	32.8	3.7	281232	2	AC130994 AC130994 Rattus no
	772	32.8	3.7	282407	2	AC114114 AC114114 Rattus no
c	773	32.8	3.7	300029	8	AE017081 AE017081 Oryza sat
	774	32.8	3.7	330939	2	AC109376 AC109376 Rattus no
c	775	32.8	3.7	347894	1	BX640431 BX640431 Bordetell
c	776	32.6	3.7	251	11	BV189099 BV189099 sqnm16236
c	777	32.6	3.7	406	6	CQ528992 CQ528992 Sequence
	778	32.6	3.7	534	3	AB035321 AB035321 Dirofilar
	779	32.6	3.7	889	5	BX933670 BX933670 Gallus ga
	780	32.6	3.7	889	5	BX935351 BX935351 Gallus ga
	781	32.6	3.7	899	5	BX935315 BX935315 Gallus ga
	782	32.6	3.7	899	5	BX936273 BX936273 Gallus ga
	783	32.6	3.7	907	8	AF159883 AF159883 Oryza sat
	784	32.6	3.7	911	5	BX933638 BX933638 Gallus ga
	785	32.6	3.7	937	5	CR352633 CR352633 Gallus ga
c	786	32.6	3.7	1695	8	AY391254 AY391254 Spumella
	787	32.6	3.7	2110	11	BV177352 BV177352 sqnm94165
	788	32.6	3.7	2110	11	BV177990 BV177990 sqnm97884
	789	32.6	3.7	2110	11	BV180345 BV180345 sqnm10903
	790	32.6	3.7	2480	10	AF013282 AF013282 Mus muscu
	791	32.6	3.7	3000	9	BC036812 BC036812 Homo sapi
	792	32.6	3.7	3421	10	AF352815 AF352815 Rattus no
c	793	32.6	3.7	4233	6	CQ850045 CQ850045 Sequence
c	794	32.6	3.7	4233	9	AK127126 AK127126 Homo sapi
	795	32.6	3.7	40933	9	AC112243 AC112243 Homo sapi
c	796	32.6	3.7	44273	9	AY623112 AY623112 Homo sapi
	797	32.6	3.7	52586	9	AF258547 AF258547 Homo sapi
c	798	32.6	3.7	57113	2	AC100045 AC100045 Mus muscu
	799	32.6	3.7	59029	9	AL445163 AL445163 Human DNA
c	800	32.6	3.7	67442	2	AC132207 AC132207 Homo sapi
c	801	32.6	3.7	94949	9	AY623115 AY623115 Homo sapi
c	802	32.6	3.7	104726	9	AC008087 AC008087 Homo sapi
	803	32.6	3.7	106873	14	AB096160 AB096160 Cercopith
	804	32.6	3.7	108299	10	AL606747 AL606747 Mouse DNA
c	805	32.6	3.7	110000	1	CR628336_13 Continuation (14 o
c	806	32.6	3.7	110000	8	CR382128_23 Continuation (24 o
	807	32.6	3.7	116004	9	AF258545 AF258545 Homo sapi
c	808	32.6	3.7	118047	9	HSDJ513M9 AL049631 Human DNA
	809	32.6	3.7	126712	9	AL137077 AL137077 Human DNA
c	810	32.6	3.7	131112	9	AL157712 AL157712 Homo sapi
	811	32.6	3.7	136002	9	AC120024 AC120024 Homo sapi
	812	32.6	3.7	142956	8	AP004641 AP004641 Oryza sat
c	813	32.6	3.7	145410	9	AC027455 AC027455 Homo sapi
c	814	32.6	3.7	146805	2	AL450424 AL450424 Homo sapi
	815	32.6	3.7	152574	9	AC011195 AC011195 Homo sapi
	816	32.6	3.7	155539	9	AL138721 AL138721 Human DNA
	817	32.6	3.7	156789	14	AF533768 AF533768 Cercopith
	818	32.6	3.7	157442	9	AC105001 AC105001 Homo sapi
c	819	32.6	3.7	157928	10	AC112256 AC112256 Mus muscu
c	820	32.6	3.7	158602	9	AL133283 AL133283 Human DNA
	821	32.6	3.7	162351	9	AC123903 AC123903 Homo sapi
	822	32.6	3.7	162456	10	AL954131 AL954131 Mouse DNA

	823	32.6	3.7	163481	9	AL139274 AL139274 Human DNA
	824	32.6	3.7	165701	8	AP004357 AP004357 Oryza sat
c	825	32.6	3.7	166233	2	AC048369 AC048369 Homo sapi
	826	32.6	3.7	167079	9	AL606489 AL606489 Human DNA
c	827	32.6	3.7	168542	2	AC058792 AC058792 Homo sapi
	828	32.6	3.7	172601	2	AC021455 AC021455 Homo sapi
	829	32.6	3.7	177303	2	AC026576 AC026576 Homo sapi
c	830	32.6	3.7	178098	9	HS168L15 AL022069 Human DNA
	831	32.6	3.7	180953	2	AC010098 AC010098 Homo sapi
c	832	32.6	3.7	183090	2	AC121175 AC121175 Rattus no
	833	32.6	3.7	184407	2	AC122767 AC122767 Mus muscu
	834	32.6	3.7	186526	10	AL596083 AL596083 Mouse DNA
c	835	32.6	3.7	187263	2	AC118725 AC118725 Mus muscu
	836	32.6	3.7	187805	9	AL356133 AL356133 Human DNA
	837	32.6	3.7	188453	9	AC025521 AC025521 Homo sapi
	838	32.6	3.7	192332	10	AL606745 AL606745 Mouse DNA
	839	32.6	3.7	200836	2	AC011965 AC011965 Homo sapi
c	840	32.6	3.7	205033	2	AC111383 AC111383 Rattus no
c	841	32.6	3.7	206504	9	AC012491 AC012491 Homo sapi
	842	32.6	3.7	212150	2	AC113078 AC113078 Mus muscu
c	843	32.6	3.7	223496	2	AL732573 AL732573 Mus muscu
c	844	32.6	3.7	234882	2	AC127871 AC127871 Rattus no
	845	32.6	3.7	236244	10	AC121481 AC121481 Rattus no
c	846	32.6	3.7	238408	2	AC140402 AC140402 Mus muscu
c	847	32.6	3.7	246257	2	AC128192 AC128192 Rattus no
c	848	32.6	3.7	247196	2	AC073822 AC073822 Mus muscu
	849	32.6	3.7	247588	10	AC114512 AC114512 Rattus no
c	850	32.6	3.7	264410	10	AC116119 AC116119 Mus muscu
	851	32.6	3.7	267507	2	AC126285 AC126285 Rattus no
	852	32.6	3.7	274738	2	AC094114 AC094114 Rattus no
c	853	32.6	3.7	300140	1	AP005956 AP005956 Bradyrhiz
	854	32.6	3.7	301995	1	AE016779 AE016779 Pseudomon
	855	32.6	3.7	320150	1	AP005033 AP005033 Streptomy
	856	32.6	3.7	328863	2	AL627202 AL627202 Homo sapi
	857	32.6	3.7	348525	1	BX640428 BX640428 Bordetell
c	858	32.6	3.7	348878	2	AC130911 AC130911 Rattus no
	859	32.6	3.7	348934	1	BX640417 BX640417 Bordetell
c	860	32.6	3.7	349442	1	BX640447 BX640447 Bordetell
	861	32.4	3.6	598	6	CQ600441 CQ600441 Sequence
c	862	32.4	3.6	605	11	BV161594 BV161594 RPAMMSEQ0
	863	32.4	3.6	608	3	AY119094 AY119094 Drosophil
	864	32.4	3.6	1017	10	RATRSIDB K01677 Rat brain-s
	865	32.4	3.6	1174	5	BC082123 BC082123 Xenopus l
	866	32.4	3.6	1178	10	BC004658 BC004658 Mus muscu
	867	32.4	3.6	1306	8	AY084476 AY084476 Arabidops
	868	32.4	3.6	1665	10	RATCYTA M33605 Rat cytolys
c	869	32.4	3.6	1744	9	HUMNAGT L48489 Homo sapien
	870	32.4	3.6	2320	9	AB046066 AB046066 Macaca fa
	871	32.4	3.6	2598	6	CQ600440 CQ600440 Sequence
	872	32.4	3.6	2827	6	CQ587786 CQ587786 Sequence
	873	32.4	3.6	2837	6	CQ583451 CQ583451 Sequence
c	874	32.4	3.6	3036	6	CQ807305 CQ807305 Sequence
	875	32.4	3.6	5090	8	AB062675 AB062675 Oryza sat
	876	32.4	3.6	5584	9	HSM808309 BX648162 Homo sapi
	877	32.4	3.6	19937	2	AC017980 AC017980 Drosophil
	878	32.4	3.6	36377	9	AC011531 AC011531 Homo sapi
	879	32.4	3.6	39421	2	AC133541 AC133541 Homo sapi
	880	32.4	3.6	87476	2	AC138695 AC138695 Homo sapi
c	881	32.4	3.6	91034	2	AC025911 AC025911 Mus muscu
c	882	32.4	3.6	103995	2	AC096695 AC096695 Rattus no
c	883	32.4	3.6	110000	1	AE017180_07 Continuation (8 of
	884	32.4	3.6	110000	2	AL929223_1 Continuation (2 of
	885	32.4	3.6	110000	2	AL929223_4 Continuation (5 of
	886	32.4	3.6	110000	8	CR380952_07 Continuation (8 of
c	887	32.4	3.6	116986	2	AC150107 Gallus ga
c	888	32.4	3.6	118300	9	AP000560 AP000560 Homo sapi
	889	32.4	3.6	123931	9	AC011404 AC011404 Homo sapi
	890	32.4	3.6	125406	9	AC008614 AC008614 Homo sapi
c	891	32.4	3.6	125726	2	AC150133 AC150133 Gallus ga
	892	32.4	3.6	129320	9	HSDJ47M23 AL096816 Human DNA
	893	32.4	3.6	135545	10	MMHC213L3 AF109905 Mus muscu
c	894	32.4	3.6	135653	9	AC130404 AC130404 Homo sapi
c	895	32.4	3.6	137836	5	BX545850 BX545850 Zebrafish
	896	32.4	3.6	141937	2	AC011686 AC011686 Homo sapi
	897	32.4	3.6	143244	9	AC091997 AC091997 Homo sapi
	898	32.4	3.6	145018	8	AP005828 AP005828 Oryza sat
c	899	32.4	3.6	145542	2	AC087618 AC087618 Homo sapi
c	900	32.4	3.6	146776	8	AP007223 AP007223 Oryza sat
	901	32.4	3.6	148864	9	HS358H7 Z77249 Human DNA s
c	902	32.4	3.6	151397	2	AL390249 AL390249 Homo sapi
	903	32.4	3.6	151751	2	AC023243 AC023243 Homo sapi
	904	32.4	3.6	153595	2	AP004239 AP004239 Oryza sat
	905	32.4	3.6	155958	10	AC114420 AC114420 Mus muscu
	906	32.4	3.6	157347	2	CR388068 CR388068 Danio rer
c	907	32.4	3.6	158800	2	AC027090 AC027090 Homo sapi
	908	32.4	3.6	161985	10	AL592169 AL592169 Mouse DNA
	909	32.4	3.6	164501	3	AC006494 AC006494 Drosophil
c	910	32.4	3.6	164686	4	AC098686 AC098686 Bos tauru
	911	32.4	3.6	165590	4	AC092858 AC092858 Bos tauru
	912	32.4	3.6	166530	9	AC069259 AC069259 Homo sapi
c	913	32.4	3.6	169168	5	BX546502 BX546502 Zebrafish
	914	32.4	3.6	173978	2	AC020649 AC020649 Homo sapi
c	915	32.4	3.6	178427	2	AC123679 AC123679 Mus muscu
	916	32.4	3.6	179562	3	AC008196 AC008196 Drosophil
c	917	32.4	3.6	187341	2	AC024980 AC024980 Homo sapi
	918	32.4	3.6	188165	9	CNS00003 AL049781 Human chr
	919	32.4	3.6	188558	2	AC150868 AC150868 Bos tauru
c	920	32.4	3.6	189762	9	AC022025 AC022025 Homo sapi
	921	32.4	3.6	189953	2	AP004844 AP004844 Oryza sat
	922	32.4	3.6	190088	10	AC132446 AC132446 Mus muscu
c	923	32.4	3.6	191110	2	AC121413 AC121413 Rattus no
c	924	32.4	3.6	191630	9	AC022239 AC022239 Homo sapi
	925	32.4	3.6	191732	4	AC096629 AC096629 Bos tauru
	926	32.4	3.6	192252	10	AL672147 AL672147 Mouse DNA
c	927	32.4	3.6	201143	9	HS150C2 AL022318 Human DNA
	928	32.4	3.6	202572	2	AC116942 AC116942 Pan trogl
	929	32.4	3.6	202911	2	AC119063 AC119063 Pan trogl
	930	32.4	3.6	207025	2	AC138843 AC138843 Homo sapi
c	931	32.4	3.6	211452	2	AP002010 AP002010 Homo sapi
	932	32.4	3.6	213613	2	AC013405 AC013405 Homo sapi
c	933	32.4	3.6	214847	2	AC098980 AC098980 Rattus no
	934	32.4	3.6	217594	1	AP002086 AP002086 Agrobacte
	935	32.4	3.6	217819	2	AC026386 AC026386 Mus muscu
c	936	32.4	3.6	219076	10	AL731713 AL731713 Mouse DNA
	937	32.4	3.6	220710	2	AC125304 AC125304 Rattus no
	938	32.4	3.6	221553	10	AC149282 AC149282 Mus muscu
	939	32.4	3.6	221899	10	AC087117 AC087117 Mus muscu
	940	32.4	3.6	224548	3	AE003739 AE003739 Drosophil
	941	32.4	3.6	228242	2	AC109115 AC109115 Rattus no
c	942	32.4	3.6	228698	2	AC127479 AC127479 Mus muscu
c	943	32.4	3.6	230157	9	AP001324 AP001324 Homo sapi
	944	32.4	3.6	230444	2	AC109424 AC109424 Rattus no
	945	32.4	3.6	232503	2	AC098900 AC098900 Rattus no
c	946	32.4	3.6	233229	2	AC108610 AC108610 Rattus no
	947	32.4	3.6	233489	2	AC097798 AC097798 Rattus no
c	948	32.4	3.6	237653	2	AC073760 AC073760 Mus muscu
c	949	32.4	3.6	239681	2	AC128835 AC128835 Rattus no
	950	32.4	3.6	245482	2	AC098630 AC098630 Rattus no
	951	32.4	3.6	251150	2	AC118390 AC118390 Rattus no
	952	32.4	3.6	251180	2	AC095821 AC095821 Rattus no
	953	32.4	3.6	275443	2	AC096407 AC096407 Rattus no
	954	32.4	3.6	300242	1	AE016790 AE016790 Pseudomon
	955	32.4	3.6	305225	2	AC130763 AC130763 Rattus no
c	956	32.4	3.6	315395	2	AC132017 AC132017 Rattus no
c	957	32.2	3.6	615	11	BV015449 BV015449 S210P6121
c	958	32.2	3.6	761	10	BC052783 BC052783 Mus muscu
c	959	32.2	3.6	796	10	BC038517 BC038517 Mus muscu
	960	32.2	3.6	863	6	A85839 A85839 Sequence 49
	961	32.2	3.6	863	6	AR155332 AR155332 Sequence
	962	32.2	3.6	863	6	E65857 E65857 Genome DNA
	963	32.2	3.6	2501	6	CQ595904 CQ595904 Sequence
	964	32.2	3.6	3143	3	AF100776 AF100776 Leishmani
c	965	32.2	3.6	3381	3	AF126442 AF126442 Lymantria
	966	32.2	3.6	5336	5	AY382882 AY382882 Gallus ga
	967	32.2	3.6	14461	6	AX256438 AX256438 Sequence
	968	32.2	3.6	37675	2	AC018116 AC018116 Drosophil

969	32.2	3.6	42265	9	AC007136	AC007136 Homo sapi
c 970	32.2	3.6	51267	2	AC100027	AC100027 Mus muscu
971	32.2	3.6	87692	9	AC011396	AC011396 Homo sapi
972	32.2	3.6	105807	8	AC006085	AC006085 Arabidops
c 973	32.2	3.6	105818	2	AC149018	AC149018 Sphoeroid
974	32.2	3.6	110000	1	AE016822_15	Continuation (16 o
975	32.2	3.6	110000	1	AE016822_16	Continuation (17 o
c 976	32.2	3.6	110000	1	AE016822_17	Continuation (18 o
c 977	32.2	3.6	110000	8	CR382127_13	Continuation (14 o
978	32.2	3.6	110000	8	CR382130_09	Continuation (10 o
979	32.2	3.6	110000	8	AE016820_11	Continuation (12 o
980	32.2	3.6	125032	9	AC007099	AC007099 Homo sapi
981	32.2	3.6	133687	2	AC002093	AC002093 Homo sapi
982	32.2	3.6	149353	8	OSJN00153	AL662953 Oryza sat
983	32.2	3.6	150652	2	AC016535	AC016535 Homo sapi
c 984	32.2	3.6	155026	9	AL442128	AL442128 Human DNA
985	32.2	3.6	155316	2	AC114646	AC114646 Mus muscu
c 986	32.2	3.6	160088	2	AC142202	AC142202 Homo sapi
987	32.2	3.6	160180	10	AC129016	AC129016 Mus muscu
988	32.2	3.6	165395	8	AC137635	AC137635 Genomic s
989	32.2	3.6	165739	9	AL353728	AL353728 Human DNA
c 990	32.2	3.6	167777	9	AC019330	AC019330 Homo sapi
c 991	32.2	3.6	168535	9	AC021302	AC021302 Homo sapi
992	32.2	3.6	169975	2	AC148813	AC148813 Rhinoloph
993	32.2	3.6	170595	2	AC025937	AC025937 Homo sapi
994	32.2	3.6	170908	9	HSBA280O9	AL121582 Human DNA
995	32.2	3.6	171525	2	AC145473	AC145473 Rattus no
996	32.2	3.6	171912	10	AC104200	AC104200 Mus muscu
997	32.2	3.6	172344	9	AC092623	AC092623 Homo sapi
998	32.2	3.6	172942	2	AC150455	AC150455 Callithri
999	32.2	3.6	173133	2	AC016166	AC016166 Homo sapi
c1000	32.2	3.6	175303	2	AC024721	AC024721 Homo sapi
1001	32.2	3.6	177206	9	AC005105	AC005105 Homo sapi
c1002	32.2	3.6	177531	2	AC129120	AC129120 Rattus no
1003	32.2	3.6	177736	3	AC005714	AC005714 Drosophil
1004	32.2	3.6	179359	2	AC150630	AC150630 Zea mays
c1005	32.2	3.6	179597	9	AC068466	AC068466 Homo sapi
1006	32.2	3.6	181120	2	AC149832	AC149832 Zea mays
1007	32.2	3.6	181577	8	AF480497	AF480497 Oryza sat
c1008	32.2	3.6	181706	9	AC114814	AC114814 Homo sapi
c1009	32.2	3.6	183228	9	AC010547	AC010547 Homo sapi
1010	32.2	3.6	185795	10	AC127333	AC127333 Mus muscu
c1011	32.2	3.6	190670	5	BX000521	BX000521 Zebrafish
1012	32.2	3.6	191041	10	AL772261	AL772261 Mouse DNA
1013	32.2	3.6	191467	3	AC008348	AC008348 Drosophil
1014	32.2	3.6	193231	2	AC149202	AC149202 Macaca mu
c1015	32.2	3.6	194309	10	AC125213	AC125213 Mus muscu
c1016	32.2	3.6	195115	9	CNS01DU7	AL133168 Human chr
1017	32.2	3.6	195370	2	AC102927	AC102927 Mus muscu
1018	32.2	3.6	197426	3	CNS07EG9	AL590442 chromosom
c1019	32.2	3.6	197689	9	CNS01DWO	AL137786 Human chr
1020	32.2	3.6	206943	2	AC138848	AC138848 Homo sapi
c1021	32.2	3.6	207239	10	AC113107	AC113107 Mus muscu
1022	32.2	3.6	207901	10	AL590389	AL590389 Mouse DNA
1023	32.2	3.6	211018	3	CNS07EGC	AL590445 chromosom
c1024	32.2	3.6	211409	2	AC138366	AC138366 Mus muscu
1025	32.2	3.6	215391	2	AC120168	AC120168 Mus muscu
c1026	32.2	3.6	226820	2	AC118872	AC118872 Rattus no
c1027	32.2	3.6	228059	2	AC109886	AC109886 Rattus no
c1028	32.2	3.6	236007	2	AC114426	AC114426 Mus muscu
1029	32.2	3.6	239591	2	AC128432	AC128432 Rattus no
c1030	32.2	3.6	241714	2	AC079564	AC079564 Mus muscu
1031	32.2	3.6	242008	2	AC118601	AC118601 Mus muscu
1032	32.2	3.6	251619	2	AC140042	AC140042 Mus muscu
1033	32.2	3.6	258290	2	AC109715	AC109715 Rattus no
1034	32.2	3.6	258888	2	AC109677	AC109677 Rattus no
1035	32.2	3.6	261384	2	AC115415	AC115415 Rattus no
1036	32.2	3.6	266173	2	AC112382	AC112382 Rattus no
c1037	32.2	3.6	267565	2	AC098917	AC098917 Rattus no
c1038	32.2	3.6	276742	2	AC096514	AC096514 Rattus no
c1039	32.2	3.6	286283	10	AC139214	AC139214 Mus muscu
1040	32.2	3.6	290655	2	AC117649	AC117649 Mus muscu
1041	32.2	3.6	300100	1	SCO939123	AL939123 Streptomy
1042	32.2	3.6	307323	3	AE003457	AE003457 Drosophil
c1043	32	3.6	338	6	CQ491357	CQ491357 Sequence
c1044	32	3.6	338	6	CQ497229	CQ497229 Sequence
1045	32	3.6	341	6	CQ473232	CQ473232 Sequence
1046	32	3.6	342	6	CQ482401	CQ482401 Sequence
1047	32	3.6	394	6	CQ503521	CQ503521 Sequence
1048	32	3.6	394	6	CQ512353	CQ512353 Sequence
1049	32	3.6	522	8	AB181185	AB181185 Populus n
1050	32	3.6	522	8	AB181239	AB181239 Populus n
1051	32	3.6	891	5	BX931809	BX931809 Gallus ga
1052	32	3.6	943	5	BX929572	BX929572 Gallus ga
c1053	32	3.6	1080	3	BMU16030	U16030 Brugia mala
c1054	32	3.6	1151	3	UOP241807	AJ241807 Opecoelid
c1055	32	3.6	1161	3	UOP241808	AJ241808 Opecoelid
1056	32	3.6	1276	1	AF246395	AF246395 Acidithio
c1057	32	3.6	1306	6	AR509408	AR509408 Sequence
c1058	32	3.6	1320	6	AR380703	AR380703 Sequence
c1059	32	3.6	1320	9	HUMSQAUSYN	L06070 Human squal
1060	32	3.6	1345	5	BC068437	BC068437 Danio rer
c1061	32	3.6	1349	6	I32887	I32887 Sequence 5
1062	32	3.6	1590	9	AY007159	AY007159 Homo sapi
1063	32	3.6	1637	4	AY339977	AY339977 Canis fam
c1064	32	3.6	1647	6	CQ716605	CQ716605 Sequence
c1065	32	3.6	1649	9	HUMSQUAL	L06105 Human hepat
c1066	32	3.6	1664	9	BC029641	BC029641 Homo sapi
c1067	32	3.6	1673	9	S76822	S76822 squalene sy
1068	32	3.6	1688	8	AF110227	AF110227 Arabidops
c1069	32	3.6	1700	9	BC009251	BC009251 Homo sapi
c1070	32	3.6	1900	6	CQ490937	CQ490937 Sequence
c1071	32	3.6	1900	6	CQ496791	CQ496791 Sequence
c1072	32	3.6	1952	9	AK057726	AK057726 Homo sapi
c1073	32	3.6	2051	9	HSSQUSYN	X69141 H.sapiens m
c1074	32	3.6	2405	8	AK101199	AK101199 Oryza sat
1075	32	3.6	2475	1	ECORECEA	M24905 Escherichia
c1076	32	3.6	3672	5	AF036942	AF036942 Gallus ga
c1077	32	3.6	4428	6	CQ614676	CQ614676 Sequence
c1078	32	3.6	4431	3	AY058795	AY058795 Drosophil
c1079	32	3.6	4439	3	AF327844	AF327844 Drosophil
1080	32	3.6	4871	6	BD262979	BD262979 DNA seque
1081	32	3.6	4871	6	AX024273	AX024273 Sequence
1082	32	3.6	6500	1	RSPYPPCL	AJ002398 Rhodobact
1083	32	3.6	7042	6	CQ614675	CQ614675 Sequence
1084	32	3.6	10501	1	AE005371	AE005371 Escherich
1085	32	3.6	10732	6	E32986	E32986 Gene encodi
c1086	32	3.6	16280	3	CET05G11	AL023816 Caenorhab
c1087	32	3.6	18700	1	D90774	D90774 E.coli geno
c1088	32	3.6	33077	9	AC148474	AC148474 Pan trogl
1089	32	3.6	35865	9	AC011552	AC011552 Homo sapi
1090	32	3.6	36685	2	AC137637	AC137637 Homo sapi
c1091	32	3.6	36868	2	AC137493	AC137493 Homo sapi
1092	32	3.6	37480	2	AC137812	AC137812 Homo sapi
c1093	32	3.6	39732	9	AC137527	AC137527 Homo sapi
1094	32	3.6	46791	9	AC004699	AC004699 Homo sapi
c1095	32	3.6	70282	9	AP001505	AP001505 Homo sapi
c1096	32	3.6	74685	2	AC114682	AC114682 Homo sapi
1097	32	3.6	76571	2	AC011649	AC011649 Homo sapi
1098	32	3.6	81147	9	AL606504	AL606504 Human DNA
1099	32	3.6	105589	2	AC092269	AC092269 Homo sapi
c1100	32	3.6	106018	9	HS864I18	AL031293 Human DNA
c1101	32	3.6	110000	1	U00096_14	Continuation (15 o
c1102	32	3.6	110000	2	AC151837_0	AC151837 Mus muscu
c1103	32	3.6	118339	8	AP003962	AP003962 Oryza sat
1104	32	3.6	121698	9	AC073578	AC073578 Homo sapi
c1105	32	3.6	122175	2	BS000631	BS000631 Pan trogl
c1106	32	3.6	123721	2	OSJN01008	AL607100 Oryza sat
1107	32	3.6	132641	9	AP000679	AP000679 Homo sapi
c1108	32	3.6	134401	10	AC125397	AC125397 Mus muscu
1109	32	3.6	138159	9	AL138965	AL138965 Human DNA
1110	32	3.6	145630	9	AL512622	AL512622 Human DNA
c1111	32	3.6	148252	2	AC135789	AC135789 Homo sapi
c1112	32	3.6	148947	8	AP004397	AP004397 Oryza sat
c1113	32	3.6	148973	2	AC149885	AC149885 Xenopus t
c1114	32	3.6	154019	2	AC137542	AC137542 Felis cat

1115	32	3.6	154730	3	AC008184	AC008184 Drosophil
1116	32	3.6	154840	2	AC032035	AC032035 Homo sapi
1117	32	3.6	157233	9	AC087564	AC087564 Homo sapi
c1118	32	3.6	159237	2	AC138328	AC138328 Mus muscu
c1119	32	3.6	161600	10	BX004866	BX004866 Mouse DNA
c1120	32	3.6	163186	2	AC027722	AC027722 Homo sapi
1121	32	3.6	166335	2	AC010313	AC010313 Homo sapi
c1122	32	3.6	166847	9	AC008393	AC008393 Homo sapi
c1123	32	3.6	166935	2	AC105335	AC105335 Mus muscu
1124	32	3.6	167136	8	AC144452	AC144452 Oryza sat
1125	32	3.6	167398	9	AC069227	AC069227 Homo sapi
1126	32	3.6	167498	2	AC148191	AC148191 Otolemur
c1127	32	3.6	168062	2	AC012857	AC012857 Drosophil
1128	32	3.6	171127	9	AC009152	AC009152 Homo sapi
1129	32	3.6	171266	9	AF404777	AF404777 Homo sapi
1130	32	3.6	172479	3	AC006590	AC006590 Drosophil
1131	32	3.6	172811	2	AC145847	AC145847 Canis fam
1132	32	3.6	173071	9	AC009477	AC009477 Homo sapi
1133	32	3.6	174435	2	AC102888	AC102888 Mus muscu
c1134	32	3.6	175649	2	AC080163	AC080163 Homo sapi
c1135	32	3.6	181105	2	AP002394	AP002394 Homo sapi
c1136	32	3.6	181532	9	CNS01DW2	AL136298 Human chr
c1137	32	3.6	181548	10	AC116326	AC116326 Mus muscu
1138	32	3.6	182166	9	AL451085	AL451085 Human DNA
c1139	32	3.6	188249	2	AC009146	AC009146 Homo sapi
1140	32	3.6	190766	9	AP001360	AP001360 Homo sapi
1141	32	3.6	191314	2	AC147697	AC147697 Callithri
c1142	32	3.6	194763	2	AC150852	AC150852 Bos tauru
c1143	32	3.6	195189	2	AC034149	AC034149 Homo sapi
c1144	32	3.6	195220	2	AC105945	AC105945 Mus muscu
1145	32	3.6	195554	2	AL714009	AL714009 Mus muscu
c1146	32	3.6	195791	2	AC018997	AC018997 Homo sapi
c1147	32	3.6	196018	2	AP001364	AP001364 Homo sapi
1148	32	3.6	196258	2	AC102839	AC102839 Mus muscu
c1149	32	3.6	196260	2	AC112606	AC112606 Rattus no
c1150	32	3.6	197000	2	AC124859	AC124859 Homo sapi
1151	32	3.6	197799	2	AC137404	AC137404 Rattus no
1152	32	3.6	199548	8	ATCHRIV45	AL161545 Arabidops
1153	32	3.6	201471	8	ATFCA7	Z97342 Arabidopsis
c1154	32	3.6	203301	2	AC147067	AC147067 Homo sapi
1155	32	3.6	203793	10	AL928796	AL928796 Mouse DNA
c1156	32	3.6	205129	2	AC148031	AC148031 Homo sapi
c1157	32	3.6	209383	10	AC121604	AC121604 Mus muscu
c1158	32	3.6	209452	10	AL732513	AL732513 Mouse DNA
1159	32	3.6	210697	2	AC135790	AC135790 Homo sapi
c1160	32	3.6	211892	10	AL732403	AL732403 Mouse DNA
1161	32	3.6	212281	2	AC112022	AC112022 Rattus no
1162	32	3.6	212360	10	AL606908	AL606908 Mouse DNA
c1163	32	3.6	214848	2	AC100561	AC100561 Mus muscu
1164	32	3.6	215348	2	AC113034	AC113034 Mus muscu
1165	32	3.6	219473	2	AC137478	AC137478 Rattus no
c1166	32	3.6	220006	2	AC084068	AC084068 Mus muscu
1167	32	3.6	220430	2	AC095315	AC095315 Rattus no
1168	32	3.6	222040	2	AC098532	AC098532 Rattus no
1169	32	3.6	226013	2	AC073680	AC073680 Mus muscu
1170	32	3.6	228610	2	AC129378	AC129378 Rattus no
1171	32	3.6	232234	10	AC118006	AC118006 Mus muscu
c1172	32	3.6	232631	2	AC136122	AC136122 Rattus no
1173	32	3.6	236533	2	AC103433	AC103433 Rattus no
1174	32	3.6	238056	2	AC105894	AC105894 Rattus no
c1175	32	3.6	239467	2	AC111384	AC111384 Rattus no
1176	32	3.6	241538	2	AC148049	AC148049 Otolemur
c1177	32	3.6	243440	2	AC098290	AC098290 Rattus no
1178	32	3.6	246184	2	AC091385	AC091385 Rattus no
c1179	32	3.6	246893	2	AC132513	AC132513 Rattus no
1180	32	3.6	251510	2	AC093337	AC093337 Mus muscu
c1181	32	3.6	255881	2	AC102994	AC102994 Rattus no
1182	32	3.6	256900	2	AC104216	AC104216 Mus muscu
1183	32	3.6	260027	3	AE003659	AE003659 Drosophil
c1184	32	3.6	263701	2	AC094442	AC094442 Rattus no
c1185	32	3.6	265103	2	AC129636	AC129636 Rattus no
c1186	32	3.6	279105	2	AL732444	AL732444 Homo sapi
c1187	32	3.6	281857	2	AC114109	AC114109 Rattus no
c1188	32	3.6	288323	2	AC140887	AC140887 Homo sapi
c1189	32	3.6	291136	1	AP002556	AP002556 Escherich
c1190	32	3.6	297050	1	AP006569	AP006569 Gloeobact
c1191	32	3.6	299350	1	AP005370	AP005370 Thermosyn
c1192	32	3.6	300900	1	AP005939	AP005939 Bradyrhiz
c1193	32	3.6	326336	2	AC046137	AC046137 Homo sapi
c1194	32	3.6	340000	9	HS21C101	AL163301 Homo sapi
1195	32	3.6	349498	1	AP003002	AP003002 Mesorhizo
1196	31.8	3.6	275	6	AX896277	AX896277 Sequence
1197	31.8	3.6	275	6	BD031810	BD031810 Sequence
1198	31.8	3.6	472	11	G28372	G28372 human STS S
1199	31.8	3.6	507	11	BV132018	BV132018 PZA00509
1200	31.8	3.6	520	6	AX658738	AX658738 Sequence
c1201	31.8	3.6	568	6	AX387595	AX387595 Sequence
1202	31.8	3.6	846	5	BX932038	BX932038 Gallus ga
c1203	31.8	3.6	1020	6	AX211275	AX211275 Sequence
1204	31.8	3.6	1032	6	E03394	E03394 DNA encodin
1205	31.8	3.6	1132	5	CR761163	CR761163 Xenopus t
c1206	31.8	3.6	1256	6	CQ715176	CQ715176 Sequence
c1207	31.8	3.6	1292	6	E44184	E44184 N-Acetylglu
c1208	31.8	3.6	1292	9	AF141315	AF141315 Homo sapi
1209	31.8	3.6	1572	1	MYNAPH	D10463 Mycoplana r
c1210	31.8	3.6	1694	8	AY312576	AY312576 Larrea tr
c1211	31.8	3.6	1724	8	AY312575	AY312575 Larrea tr
c1212	31.8	3.6	2015	6	AR535228	AR535228 Sequence
c1213	31.8	3.6	2015	6	AX398994	AX398994 Sequence
c1214	31.8	3.6	2015	6	AX774825	AX774825 Sequence
c1215	31.8	3.6	2015	6	AX781549	AX781549 Sequence
c1216	31.8	3.6	2015	6	AX960774	AX960774 Sequence
c1217	31.8	3.6	2015	9	HUMTAXREBA	D90209 Homo sapien
c1218	31.8	3.6	2019	6	AR531626	AR531626 Sequence
1219	31.8	3.6	2490	6	AX833076	AX833076 Sequence
1220	31.8	3.6	2490	9	AK094505	AK094505 Homo sapi
c1221	31.8	3.6	10672	1	AE004979	AE004979 Halobacte
1222	31.8	3.6	11251	1	AE005560	AE005560 Escherich
c1223	31.8	3.6	12217	1	AE004520	AE004520 Pseudomon
1224	31.8	3.6	13654	1	AE005754	AE005754 Caulobact
c1225	31.8	3.6	16234	1	AE001060	AE001060 Archaeogl
c1226	31.8	3.6	18586	2	AC019879	AC019879 Drosophil
c1227	31.8	3.6	26100	3	DMC190E7	AL022017 Drosophil
1228	31.8	3.6	36210	9	AY323826	AY323826 Homo sapi
c1229	31.8	3.6	43744	9	AC006048	AC006048 Homo sapi
c1230	31.8	3.6	49999	6	AX015917	AX015917 Sequence
1231	31.8	3.6	56131	9	AP000295	AP000295 Homo sapi
1232	31.8	3.6	58846	9	BX470206	BX470206 Human DNA
1233	31.8	3.6	62498	2	AC136490	AC136490 Homo sapi
c1234	31.8	3.6	67884	2	AC115103	AC115103 Homo sapi
1235	31.8	3.6	69495	9	BX322539	BX322539 Human DNA
c1236	31.8	3.6	72243	9	AL731858	AL731858 Human DNA
1237	31.8	3.6	83547	2	AC022890	AC022890 Homo sapi
1238	31.8	3.6	88721	2	AC021952	AC021952 Mus muscu
1239	31.8	3.6	90837	10	AL928648	AL928648 Mouse DNA
c1240	31.8	3.6	93471	9	AL592486	AL592486 Human DNA
c1241	31.8	3.6	95579	9	AC023162	AC023162 Homo sapi
1242	31.8	3.6	98356	9	HS344J2	AL449213 Homo sapi
1243	31.8	3.6	100000	9	AP000044	AP000044 Homo sapi
1244	31.8	3.6	100000	9	AP000112	AP000112 Homo sapi
1245	31.8	3.6	100000	9	AP000188	AP000188 Homo sapi
c1246	31.8	3.6	100000	9	AP000509	AP000509 Homo sapi
c1247	31.8	3.6	100020	9	AC092165	AC092165 Homo sapi
1248	31.8	3.6	100046	5	BX537250	BX537250 Zebrafish
c1249	31.8	3.6	100272	9	HSDJ842G6	AL109657 Human DNA
1250	31.8	3.6	104171	2	AC019499	AC019499 Drosophil
1251	31.8	3.6	107652	9	HSDJ259N9	AL078477 Human DNA
1252	31.8	3.6	110000	1	AE017282_08	Continuation (9 of
c1253	31.8	3.6	110000	1	AE017282_25	Continuation (26 o
c1254	31.8	3.6	110000	1	AP006840_16	Continuation (17 o
c1255	31.8	3.6	110000	2	AC140148_2	Continuation (3 of
c1256	31.8	3.6	110107	2	CR847781	CR847781 Homo sapi
1257	31.8	3.6	115045	9	AC004414	AC004414 Homo sapi
1258	31.8	3.6	117951	9	AC023049	AC023049 Homo sapi
1259	31.8	3.6	121659	9	CR388229	CR388229 Human DNA
c1260	31.8	3.6	124343	9	AL357127	AL357127 Human DNA

1261	31.8	3.6	124717	5	BX572635	BX572635 Zebrafish
c1262	31.8	3.6	124876	9	AC004167	AC004167 Homo sapi
c1263	31.8	3.6	135105	8	CNS08CA8	AL831795 Oryza sat
1264	31.8	3.6	138141	9	AC087653	AC087653 Homo sapi
1265	31.8	3.6	144048	9	AC013762	AC013762 Homo sapi
1266	31.8	3.6	144734	2	AC148922	AC148922 Dasypus n
1267	31.8	3.6	150645	10	AC131774	AC131774 Mus muscu
1268	31.8	3.6	151242	2	AC144589	AC144589 Homo sapi
1269	31.8	3.6	152015	2	AC130795	AC130795 Felis cat
c1270	31.8	3.6	152015	2	AC130795	AC130795 Felis cat
1271	31.8	3.6	152177	10	AL672064	AL672064 Mouse DNA
c1272	31.8	3.6	152799	2	AC150972	AC150972 Bos tauru
1273	31.8	3.6	154920	2	AC138355	AC138355 Mus muscu
1274	31.8	3.6	156426	9	AC078906	AC078906 Homo sapi
c1275	31.8	3.6	156441	9	AC091869	AC091869 Homo sapi
1276	31.8	3.6	157264	10	AC132914	AC132914 Mus muscu
1277	31.8	3.6	158091	9	AC140171	AC140171 Homo sapi
1278	31.8	3.6	158276	2	AC012033	AC012033 Homo sapi
c1279	31.8	3.6	158328	2	AC130197	AC130197 Felis cat
1280	31.8	3.6	160401	9	AC009277	AC009277 Homo sapi
1281	31.8	3.6	160525	2	AC027074	AC027074 Homo sapi
c1282	31.8	3.6	164252	3	AC104288	AC104288 Drosophil
1283	31.8	3.6	164396	2	HSAC000380	AC000380 Homo sapi
c1284	31.8	3.6	166664	9	AL441992	AL441992 Human DNA
1285	31.8	3.6	166885	9	AC091873	AC091873 Homo sapi
1286	31.8	3.6	168887	9	AL662833	AL662833 Human DNA
c1287	31.8	3.6	174040	2	AC073950	AC073950 Homo sapi
1288	31.8	3.6	174073	2	AC116828	AC116828 Mus muscu
c1289	31.8	3.6	175603	10	AC115301	AC115301 Mus muscu
c1290	31.8	3.6	177725	2	AC105162	AC105162 Mus muscu
c1291	31.8	3.6	178099	2	CR392352	CR392352 Danio rer
1292	31.8	3.6	178560	10	AC134839	AC134839 Mus muscu
1293	31.8	3.6	178995	10	AL672052	AL672052 Mouse DNA
c1294	31.8	3.6	179223	2	AC141463	AC141463 Homo sapi
c1295	31.8	3.6	179745	10	AC135377	AC135377 Mus muscu
1296	31.8	3.6	179816	2	AC074188	AC074188 Homo sapi
1297	31.8	3.6	180526	2	AC145446	AC145446 Felis cat
1298	31.8	3.6	181169	2	AC118583	AC118583 Papio anu
c1299	31.8	3.6	182105	9	AC009136	AC009136 Homo sapi
c1300	31.8	3.6	182572	2	AC022738	AC022738 Homo sapi
1301	31.8	3.6	182726	2	AC084436	AC084436 Homo sapi
c1302	31.8	3.6	185162	9	AC140132	AC140132 Homo sapi
c1303	31.8	3.6	185936	2	AC139837	AC139837 Homo sapi
1304	31.8	3.6	186625	2	AC145540	AC145540 Oryctolag
c1305	31.8	3.6	191690	2	AC136907	AC136907 Rattus no
1306	31.8	3.6	193580	2	CR751222	CR751222 Homo sapi
c1307	31.8	3.6	194384	2	AC123958	AC123958 Rattus no
c1308	31.8	3.6	196669	2	BX950864	BX950864 Danio rer
1309	31.8	3.6	196967	2	AC108589	AC108589 Rattus no
c1310	31.8	3.6	197785	9	AC016057	AC016057 Homo sapi
1311	31.8	3.6	203304	10	AC126258	AC126258 Mus muscu
1312	31.8	3.6	204298	9	AL662844	AL662844 Human DNA
c1313	31.8	3.6	204644	2	AC066588	AC066588 Homo sapi
1314	31.8	3.6	205990	2	AC114161	AC114161 Rattus no
1315	31.8	3.6	207429	10	AC150312	AC150312 Mus muscu
c1316	31.8	3.6	210301	9	AF307337	AF307337 Homo sapi
1317	31.8	3.6	224215	2	AC114068	AC114068 Rattus no
c1318	31.8	3.6	228696	2	AC109757	AC109757 Rattus no
1319	31.8	3.6	228893	2	AC111848	AC111848 Rattus no
c1320	31.8	3.6	230675	10	AC144768	AC144768 Mus muscu
1321	31.8	3.6	231141	2	AC111368	AC111368 Rattus no
1322	31.8	3.6	231991	2	AC129392	AC129392 Rattus no
1323	31.8	3.6	232618	2	AC134996	AC134996 Rattus no
1324	31.8	3.6	233270	2	AC129038	AC129038 Rattus no
1325	31.8	3.6	233772	2	AC115403	AC115403 Rattus no
c1326	31.8	3.6	236687	2	AC140151	AC140151 Homo sapi
c1327	31.8	3.6	236822	9	D84394	D84394 Homo sapien
1328	31.8	3.6	236969	10	AC093467	AC093467 Mus muscu
1329	31.8	3.6	243777	2	AC131226	AC131226 Rattus no
1330	31.8	3.6	248214	2	AL138811	AL138811 Homo sapi
1331	31.8	3.6	250519	2	AC094894	AC094894 Rattus no
1332	31.8	3.6	251141	2	AC116235	AC116235 Rattus no
1333	31.8	3.6	252520	2	AC131432	AC131432 Rattus no
c1334	31.8	3.6	253991	2	AC128867	AC128867 Rattus no
c1335	31.8	3.6	263623	2	AC107560	AC107560 Rattus no
c1336	31.8	3.6	263855	2	AC127797	AC127797 Rattus no
1337	31.8	3.6	267888	1	AP002565	AP002565 Escherich
c1338	31.8	3.6	269654	2	AC098068	AC098068 Rattus no
1339	31.8	3.6	273807	2	AC025421	AC025421 Homo sapi
c1340	31.8	3.6	290885	2	AC128572	AC128572 Rattus no
c1341	31.8	3.6	301675	1	AP005027	AP005027 Streptomy
1342	31.8	3.6	301925	1	AP005046	AP005046 Streptomy
c1343	31.8	3.6	308311	3	AE003420	AE003420 Drosophil
c1344	31.8	3.6	330608	2	AC109561	AC109561 Rattus no
1345	31.8	3.6	340000	9	AP001716	AP001716 Homo sapi
1346	31.6	3.6	240	9	HSJ225716	AJ225716 Homo sapi
1347	31.6	3.6	364	6	AR425705	AR425705 Sequence
1348	31.6	3.6	364	6	AX986399	AX986399 Sequence
1349	31.6	3.6	364	6	BD121258	BD121258 EST and e
1350	31.6	3.6	474	6	CQ441019	CQ441019 Sequence
1351	31.6	3.6	559	6	AX658764	AX658764 Sequence
c1352	31.6	3.6	666	12	AY657499	AY657499 Synthetic
1353	31.6	3.6	941	6	CQ716119	CQ716119 Sequence
1354	31.6	3.6	1092	5	BC073043	BC073043 Xenopus l
1355	31.6	3.6	1115	3	AY344830	AY344830 Anopheles
c1356	31.6	3.6	1341	6	A96172	A96172 Sequence 20
1357	31.6	3.6	1390	5	BC054288	BC054288 Xenopus l
1358	31.6	3.6	1429	5	BC078059	BC078059 Xenopus l
c1359	31.6	3.6	1860	8	AF082869	AF082869 Chlamydom
c1360	31.6	3.6	1873	3	AY122624	AY122624 Dimastige
c1361	31.6	3.6	1874	6	BD223746	BD223746 Genes of
c1362	31.6	3.6	1874	6	AR428562	AR428562 Sequence
1363	31.6	3.6	1945	10	RRINT5G	X54419 R.rattus ge
1364	31.6	3.6	2011	5	CR762068	CR762068 Xenopus t
1365	31.6	3.6	2424	10	BC031923	BC031923 Mus muscu
1366	31.6	3.6	2991	6	BD139961	BD139961 Secreted
1367	31.6	3.6	3335	10	RATP130CAS	D29766 Rattus norv
1368	31.6	3.6	3462	6	CQ782989	CQ782989 Sequence
1369	31.6	3.6	3462	6	BD127415	BD127415 Primer fo
1370	31.6	3.6	3462	9	AK075002	AK075002 Homo sapi
c1371	31.6	3.6	3483	10	BC023832	BC023832 Mus muscu
1372	31.6	3.6	3486	9	BC008843	BC008843 Homo sapi
1373	31.6	3.6	3487	6	CQ783742	CQ783742 Sequence
1374	31.6	3.6	3487	6	BD127809	BD127809 Primer fo
1375	31.6	3.6	3487	9	AK074912	AK074912 Homo sapi
1376	31.6	3.6	3499	9	BC039854	BC039854 Homo sapi
c1377	31.6	3.6	3843	6	AX834567	AX834567 Sequence
c1378	31.6	3.6	3843	9	AK097105	AK097105 Homo sapi
1379	31.6	3.6	4533	6	AR106656	AR106656 Sequence
1380	31.6	3.6	4533	10	RATADCY3	M55075 R.norvegicu
1381	31.6	3.6	6949	9	AB007915	AB007915 Homo sapi
1382	31.6	3.6	7395	6	CQ588555	CQ588555 Sequence
1383	31.6	3.6	8173	14	AY593838	AY593838 Foot-and-
1384	31.6	3.6	10245	1	AE004569	AE004569 Pseudomon
c1385	31.6	3.6	12087	3	CEUNC15	X08068 Caenorhabdi
c1386	31.6	3.6	12263	9	HSFESFPS	X06292 Human c-fes
c1387	31.6	3.6	15297	6	AR183262	AR183262 Sequence
c1388	31.6	3.6	15297	6	AR456324	AR456324 Sequence
c1389	31.6	3.6	20000	9	AP001109	AP001109 Homo sapi
c1390	31.6	3.6	20604	6	CQ588554	CQ588554 Sequence
1391	31.6	3.6	32632	3	CEF07A5	Z72506 Caenorhabdi
1392	31.6	3.6	33550	9	AC003004	AC003004 Human Chr
c1393	31.6	3.6	34551	6	AX647685	AX647685 Sequence
c1394	31.6	3.6	35865	9	AC011552	AC011552 Homo sapi
c1395	31.6	3.6	36814	9	AC006127	AC006127 Homo sapi
1396	31.6	3.6	43455	3	AF036706	AF036706 Caenorhab
1397	31.6	3.6	48634	9	HS197K23	AL035465 Human DNA
1398	31.6	3.6	49413	2	AC140017	AC140017 Homo sapi
c1399	31.6	3.6	52359	2	AC010772	AC010772 Homo sapi
1400	31.6	3.6	53370	9	AL592071	AL592071 Human DNA
1401	31.6	3.6	54419	2	AC015298	AC015298 Drosophil
c1402	31.6	3.6	55237	8	CNS08CBG	AL928743 Oryza sat
c1403	31.6	3.6	58996	1	AB034704	AB034704 Rubriviva
1404	31.6	3.6	66867	2	AC073170	AC073170 Homo sapi
1405	31.6	3.6	72690	2	AC140527_3	Continuation (4 of
1406	31.6	3.6	74216	2	AC138874	AC138874 Homo sapi

c1407	31.6	3.6	77457	1	AF210249	AF210249 Streptomy
c1408	31.6	3.6	80327	2	AC135619	AC135619 Homo sapi
c1409	31.6	3.6	82183	9	HSJ1037B9	AL117377 Human DNA
1410	31.6	3.6	86748	9	AC068717	AC068717 Homo sapi
1411	31.6	3.6	89690	2	AC130664_3	Continuation (4 of
1412	31.6	3.6	96589	6	AX695671	AX695671 Sequence
c1413	31.6	3.6	97839	2	AC141520	AC141520 Rattus no
c1414	31.6	3.6	99304	9	AC106825	AC106825 Homo sapi
c1415	31.6	3.6	99576	5	BX005410	BX005410 Zebrafish
c1416	31.6	3.6	102910	9	AF254822	AF254822 Homo sapi
1417	31.6	3.6	105360	9	AC093218	AC093218 Homo sapi
1418	31.6	3.6	108661	9	AC026736	AC026736 Homo sapi
1419	31.6	3.6	109222	8	CNS08C91	AL732378 Oryza sat
1420	31.6	3.6	109529	2	AP003870	AP003870 Oryza sat
1421	31.6	3.6	110000	8	CR382127_04	Continuation (5 of
1422	31.6	3.6	110000	8	CR382127_05	Continuation (6 of
1423	31.6	3.6	117320	9	AL591896	AL591896 Human DNA
c1424	31.6	3.6	119050	9	AC127024	AC127024 Homo sapi
1425	31.6	3.6	124605	8	CNS07YPW	AL731762 Oryza sat
1426	31.6	3.6	128059	4	AY386694	AY386694 Oryctolag
c1427	31.6	3.6	129770	9	AC104684	AC104684 Homo sapi
c1428	31.6	3.6	130297	9	AC107425	AC107425 Homo sapi
1429	31.6	3.6	133689	8	AP005483	AP005483 Oryza sat
1430	31.6	3.6	135330	10	AL772165	AL772165 Mouse DNA
c1431	31.6	3.6	135417	9	HSDJ412I7	AL132795 Human DNA
c1432	31.6	3.6	135513	9	AC008454	AC008454 Homo sapi
c1433	31.6	3.6	136956	2	AC137338	AC137338 Rattus no
1434	31.6	3.6	138929	2	AC147945	AC147945 Atelerix
1435	31.6	3.6	139446	4	AY386697	AY386697 Oryctolag
c1436	31.6	3.6	143291	9	AL137792	AL137792 Human DNA
c1437	31.6	3.6	143557	9	AC011442	AC011442 Homo sapi
1438	31.6	3.6	146150	2	AC021298	AC021298 Homo sapi
c1439	31.6	3.6	147289	8	AC119072	AC119072 Oryza sat
1440	31.6	3.6	149367	8	AP004586	AP004586 Oryza sat
1441	31.6	3.6	151009	2	AC135784	AC135784 Homo sapi
1442	31.6	3.6	151498	9	AC099331	AC099331 Homo sapi
1443	31.6	3.6	152086	2	AC121444	AC121444 Rattus no
1444	31.6	3.6	152462	2	AP004653	AP004653 Oryza sat
1445	31.6	3.6	152586	9	AC016968	AC016968 Homo sapi
c1446	31.6	3.6	153292	9	AL513318	AL513318 Human DNA
1447	31.6	3.6	153295	2	AC137280	AC137280 Rattus no
1448	31.6	3.6	153520	9	AC130324	AC130324 Homo sapi
1449	31.6	3.6	155092	9	AC025774	AC025774 Homo sapi
c1450	31.6	3.6	155341	10	AC137713	AC137713 Mus muscu
c1451	31.6	3.6	156889	2	AC004586	AC004586 Homo sapi
1452	31.6	3.6	158216	9	AC092351	AC092351 Homo sapi
c1453	31.6	3.6	158257	9	AC005585	AC005585 Homo sapi
c1454	31.6	3.6	159593	9	AC004832	AC004832 Homo sapi
1455	31.6	3.6	159978	2	AC139479	AC139479 Homo sapi
1456	31.6	3.6	160982	2	AC128945	AC128945 Rattus no
c1457	31.6	3.6	162777	10	AL691457	AL691457 Mouse DNA
1458	31.6	3.6	164168	9	AL135927	AL135927 Human DNA
c1459	31.6	3.6	164179	9	AC007227	AC007227 Homo sapi
c1460	31.6	3.6	166015	2	AC119213	AC119213 Mus muscu
c1461	31.6	3.6	166390	2	AC139477	AC139477 Homo sapi
c1462	31.6	3.6	166683	10	AC099705	AC099705 Mus muscu
c1463	31.6	3.6	167075	2	AC138885	AC138885 Homo sapi
1464	31.6	3.6	167969	2	AC139474	AC139474 Homo sapi
c1465	31.6	3.6	168031	2	AC068430	AC068430 Homo sapi
c1466	31.6	3.6	168105	9	AC093815	AC093815 Homo sapi
c1467	31.6	3.6	168298	2	AC140827	AC140827 Homo sapi
c1468	31.6	3.6	168332	2	AC102039	AC102039 Mus muscu
1469	31.6	3.6	168910	5	CNS09SBV	BX629357 Tetraodon
c1470	31.6	3.6	169079	2	AC140018	AC140018 Homo sapi
c1471	31.6	3.6	169276	2	AC140818	AC140818 Homo sapi
1472	31.6	3.6	169371	2	AC138902	AC138902 Homo sapi
c1473	31.6	3.6	169946	2	AC140891	AC140891 Homo sapi
1474	31.6	3.6	170380	9	AC138965	AC138965 Homo sapi
1475	31.6	3.6	170870	10	AC142270	AC142270 Mus muscu
1476	31.6	3.6	171006	10	AC109805	AC109805 Mus muscu
c1477	31.6	3.6	171569	3	AC007811	AC007811 Drosophil
1478	31.6	3.6	171655	2	AC067919	AC067919 Homo sapi
c1479	31.6	3.6	172061	2	AC102282	AC102282 Mus muscu
1480	31.6	3.6	172868	9	AC009117	AC009117 Homo sapi
1481	31.6	3.6	174440	2	AC140010	AC140010 Homo sapi
1482	31.6	3.6	174600	2	AC139471	AC139471 Homo sapi
1483	31.6	3.6	175548	2	AC140130	AC140130 Homo sapi
1484	31.6	3.6	176994	2	AC140169	AC140169 Homo sapi
1485	31.6	3.6	178035	2	AC068680	AC068680 Homo sapi
c1486	31.6	3.6	179639	2	AC117743	AC117743 Mus muscu
c1487	31.6	3.6	179652	2	AC149616	AC149616 Papio anu
1488	31.6	3.6	179711	2	AC019312	AC019312 Homo sapi
c1489	31.6	3.6	179937	9	CNS05TCV	AL355840 Human chr
1490	31.6	3.6	180195	2	AC027089	AC027089 Homo sapi
c1491	31.6	3.6	180537	2	AC023266	AC023266 Homo sapi
1492	31.6	3.6	180725	2	AC119511	AC119511 Rattus no
1493	31.6	3.6	181277	2	AC139478	AC139478 Homo sapi
c1494	31.6	3.6	182187	2	AC109374	AC109374 Rattus no
c1495	31.6	3.6	183088	9	AC007600	AC007600 Homo sapi
1496	31.6	3.6	183190	2	AC139270	AC139270 Homo sapi
1497	31.6	3.6	183591	2	AC135777	AC135777 Homo sapi
c1498	31.6	3.6	184871	2	CR376788	CR376788 Danio rer
1499	31.6	3.6	184879	2	AC139470	AC139470 Homo sapi
c1500	31.6	3.6	185909	2	AC139468	AC139468 Homo sapi

ALIGNMENTS

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RESULT 1
AX358978
LOCUS       AX358978                890 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 231 from Patent WO0193983.
ACCESSION   AX358978
VERSION     AX358978.1  GI:18675390
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0193983-A 231 13-DEC-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 890;  DB 6;  Length 890;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-242;
  Matches  890;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
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Db         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120

Qy        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
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Db        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180

Qy        181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
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Qy        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
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Db        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300

Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
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Db        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360

Qy        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
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Db        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420

Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
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Db        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480

Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
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Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
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Db        601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660

Qy        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
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Db        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720

Qy        721 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
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Db        721 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890
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Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890


RESULT 2
AX362471
LOCUS       AX362471                890 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 231 from Patent WO0208288.
ACCESSION   AX362471
VERSION     AX362471.1  GI:18694693
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0208288-A 231 31-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 890;  DB 6;  Length 890;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-242;
  Matches  890;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
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Qy         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
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Qy        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
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Qy        181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
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Qy        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
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Db        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300

Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
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Qy        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
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Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
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Db        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480

Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
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Db        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540

Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
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Db        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600

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Qy        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
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Db        721 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
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Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890
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Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890


RESULT 3
AX454720
LOCUS       AX454720                890 bp    DNA     linear   PAT 08-JUL-2002
DEFINITION  Sequence 305 from Patent WO0208284.
ACCESSION   AX454720
VERSION     AX454720.1  GI:21713984
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 305 31-JAN-2002;
            Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
            (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
            Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
            Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
            ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
            Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
            I. (US)
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 890;  DB 6;  Length 890;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-242;
  Matches  890;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
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Db          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60

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Db        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180

Qy        181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
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Qy        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
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Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
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Db        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360

Qy        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
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Db        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420

Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
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Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
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Db        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540

Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
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Qy        601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
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Db        601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660

Qy        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
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Db        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720

Qy        721 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
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Db        721 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
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Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890
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Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890


RESULT 4
AX491198
LOCUS       AX491198                890 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 305 from Patent WO0200690.
ACCESSION   AX491198
VERSION     AX491198.1  GI:22323936
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0200690-A 305 03-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 890;  DB 6;  Length 890;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-242;
  Matches  890;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60

Qy         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
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Db         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120

Qy        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
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Qy        181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
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Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
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Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
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Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
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Db        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540

Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
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Qy        721 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
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Db        721 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
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Db        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATCAAA 890
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Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATCAAA 890


RESULT 5
AY359109
LOCUS       AY359109                890 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA92274 GWTM1933 (UNQ1933) mRNA, complete cds.
ACCESSION   AY359109
VERSION     AY359109.1  GI:37183334
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 890)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .890
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                     /db_xref="taxon:9606"
                     /clone="DNA92274"
     gene            1. .890
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     CDS             89. .760
                     /locus_tag="UNQ1933"
                     /note="PRO4408"
                     /codon_start=1
                     /product="GWTM1933"
                     /protein_id="AAQ89467.1"
                     /db_xref="GI:37183335"
                     /translation="MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQ
                     GLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSR
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                     KTRQR"
ORIGIN

  Query Match           100.0%;  Score 890;  DB 9;  Length 890;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-242;
  Matches  890;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
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Db          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60

Qy         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
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Db         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120

Qy        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
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Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
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Db        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360

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Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
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Db        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480

Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540

Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
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Db        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600

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Qy        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
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Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
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Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890
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Db        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAAATCATCAAA 890


RESULT 6
BC020779
LOCUS       BC020779                914 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens hypothetical protein MGC22776, mRNA (cDNA clone
            MGC:22776 IMAGE:4700840), complete cds.
ACCESSION   BC020779
VERSION     BC020779.1  GI:18088479
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 914)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 36 Row: p Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21450646.
FEATURES             Location/Qualifiers
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                     /db_xref="GI:18088480"
                     /db_xref="LocusID:157310"
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                     AEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGK
                     VISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKH
                     KTRRR"
ORIGIN

  Query Match           98.7%;  Score 878.2;  DB 9;  Length 914;
  Best Local Similarity  99.7%;  Pred. No. 1.2e-238;
  Matches  880;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 ACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCT 64
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Db          1 ACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCT 60

Qy         65 CCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG 124
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Db         61 CCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTTACAGCAGCACTG 120

Qy        125 TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCAT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCAT 180

Qy        185 GAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAG 240

Qy        245 TTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACC 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACC 300

Qy        305 TCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTG 364
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Db        301 TCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTG 360

Qy        365 GTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACAT 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACAT 420

Qy        425 TGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAG 484
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        421 TGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAGGAG 480

Qy        485 TTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTC 540

Qy        545 TTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGA 600

Qy        605 GGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGC 660

Qy        665 ACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGG 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGG 720

Qy        725 GCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTG 784
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
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Db        721 GCCAGCGAGCCCAAGCACAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTG 780

Qy        785 CCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTG 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTG 840

Qy        845 GATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATC 887
              |||||||||||||||||||||||||||||||||||||||||||
Db        841 GATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATC 883


RESULT 7
AX060293
LOCUS       AX060293                 932 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 1 from Patent WO0078802.
ACCESSION   AX060293
VERSION     AX060293.1  GI:12405782
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A., Fernandes,E., Vernet,C., Yang,M., Boldog,F.L. and
            Herrmann,J.L.
  TITLE     Secreted polypeptides and corresponding polynucleotides
  JOURNAL   Patent: WO 0078802-A 1 28-DEC-2000;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .932
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             113. .796
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC24866.1"
                     /db_xref="GI:12405783"
                     /translation="MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQ
                     GLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSR
                     AEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGK
                     VISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKH
                     KNQAEIAAC"
ORIGIN

  Query Match             97.2%;  Score 865.2;  DB 6;  Length 932;
  Best Local Similarity   99.0%;  Pred. No. 6e-235;
  Matches  881;  Conservative    0;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||
Db         25 AAGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCC 84

Qy         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 144

Qy        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 204

Qy        181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 264

Qy        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 324

Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 384

Qy        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 444

Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        445 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCA 504

Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 564

Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 624

Qy        601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        625 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGC 684

Qy        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGA 744

Qy        721 AAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGG 779
              ||||||||||||||||||||| |||||||||| |||||||||||||||||||||||||
Db        745 AAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGG 804

Qy        780 CTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCC 839
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        805 CTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCC 864

Qy        840 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATCAA 889
              |||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        865 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCATCCA 914


RESULT 8
AX083422
LOCUS       AX083422                 897 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 114 from Patent WO0112660.
ACCESSION   AX083422
VERSION     AX083422.1  GI:13185262
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 114 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .897
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             99. .782
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC33305.1"
                     /db_xref="GI:13185263"
                     /translation="MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQ
                     GLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSR
                     AEPRQRFWRHWLVTDIKGADLKKGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGK
                     VISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKH
                     KNQAEIAAC"
ORIGIN

  Query Match             96.4%;  Score 857.8;  DB 6;  Length 897;
  Best Local Similarity   99.1%;  Pred. No. 7.7e-233;
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  Matches  873;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| |||
Db         11 AAGTACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCC 70

Qy         61 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC 130

Qy        121 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC 190

Qy        181 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC 250

Qy        241 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGAT 310

Qy        301 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT 370

Qy        361 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG 430

Qy        421 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 480
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Db        431 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA 490

Qy        481 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA 550

Qy        541 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC 610

Qy        601 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
              ||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
Db        611 TCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGC 670

Qy        661 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 AAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGA 730

Qy        721 AAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGG 779
              |||||||||||||||||||||| |||||||||| |||||||||||||||||||||||||
Db        731 AAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGG 790

Qy        780 CTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCC 839
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        791 CTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCC 850

Qy        840 CTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||||||||||||||||| |||||||||
Db        851 CTCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAA 891


RESULT 9
BD248885
LOCUS       BD248885               1028 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  47 human secreted proteins.
ACCESSION   BD248885
VERSION     BD248885.1  GI:33058655
KEYWORDS    JP 2002532083-A/55.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1028)
  AUTHORS   Ruben,S.M., Ebner,R., Rosen,C.A., Endress,G.A., Soppet,D.R., Ni,J.,
            Duan,R.D., Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S. and
            Florence,K.
  TITLE     47 human secreted proteins
  JOURNAL   Patent: JP 2002532083-A 55 02-OCT-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002532083-A/55
            PD   02-OCT-2002
            PF   16-DEC-1999 JP 2000588195
            PR   17-DEC-1998 US    60/112809,18-DEC-1998 US    60/113006 PI
            STEVEN M RUBEN,REINHARD EBNER,CRAIG A ROSEN,GREGORY A ENDRESS, PI
            DANIEL R SOPPET,JIAN NI,ROXANNE D DUAN,PAUL
            A MOORE,YANGGU SHI,
            PI   DAVID W LAFLEUR,HENRIK S OLSEN,KIMBERLY FLORENCE PC
            C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P1/00,A61P1/04, PC
            A61P3/02,
            PC   A61P25/00,A61P25/14,A61P25/16,A61P25/18,A61P25/28,A61P29/00,
            PC   A61P35/00,
            PC   A61P37/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12Q1/02,G01N33/15,G01N33/50,C12N15/00, PC
             A61K37/02,
            PC   C12N5/00
            CC   n equals a,t,g, or c
            CC   n equals a,t,g, or c
            CC   n equals a,t,g, or c
            CC   n equals a,t,g, or c
            FH   Key             Location/Qualifiers
            FT   source          1. .1028
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           93.6%;  Score 833.2;  DB 6;  Length 1028;
  Best Local Similarity   99.0%;  Pred. No. 7.8e-226;
  Matches  857;  Conservative    2;  Mismatches    5;  Indels    2;  Gaps    2;

Qy         17 GTGGTGGACTGGATTAGCTGCGGA-GCCCTGGAAGCTGCCTGTCCTTCTCCCTGTGCTTA 75
              | |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         80 GAGGTGGACTGGATTAGCTGCGGAGGCCCTGGAAGCTGCCTGTCCTTCTCCCTGTGCTTA 139

Qy         76 ACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCT 199

Qy        136 CATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTT 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 CATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTT 259

Qy        196 GGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACAT 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACAT 319

Qy        256 TGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGA 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGA 379

Qy        316 GCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGA 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 GCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGA 439

Qy        376 TCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAAC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 TCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAAC 499

Qy        436 AGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTA 495
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                ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        500 AGATATCAAGGGCGCCGACCTGAAGRAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTA 559

Qy        496 CCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCT 555
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 CCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCT 619

Qy        556 TCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAA 615
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Db        620 TCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAA 679

Qy        616 AATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCAT 675
                ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        680 AATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCAT 739

Qy        676 GACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCC 735
                |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        740 GACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCC 799

Qy        736 CAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGC 794
                ||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        800 CAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGC 859

Qy        795 ATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAAC 854
                ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        860 ATGTGGCCACACTGCYCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAAC 919

Qy        855 CCCTTCTTTTCCAAATTAAAAAAAAA 880
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Db        920 CCCTTCTTTTCCAAATAAAAAAAAAA 945


RESULT 10
BD248890
LOCUS       BD248890                952 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  47 human secreted proteins.
ACCESSION   BD248890
VERSION     BD248890.1  GI:33058660
KEYWORDS    JP 2002532083-A/60.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 952)
  AUTHORS   Ruben,S.M., Ebner,R., Rosen,C.A., Endress,G.A., Soppet,D.R., Ni,J.,
            Duan,R.D., Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S. and
            Florence,K.
  TITLE     47 human secreted proteins
  JOURNAL   Patent: JP 2002532083-A 60 02-OCT-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002532083-A/60
            PD   02-OCT-2002
            PF   16-DEC-1999 JP 2000588195
            PR   17-DEC-1998 US    60/112809,18-DEC-1998 US    60/113006 PI
            STEVEN M RUBEN,REINHARD EBNER,CRAIG A ROSEN,GREGORY A ENDRESS, PI
            DANIEL R SOPPET,JIAN NI,ROXANNE D DUAN,PAUL
            A MOORE,YANGGU SHI,
            PI   DAVID W LAFLEUR,HENRIK S OLSEN,KIMBERLY FLORENCE PC
            C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P1/00,A61P1/04, PC
            A61P3/02,
            PC   A61P25/00,A61P25/14,A61P25/16,A61P25/18,A61P25/28,A61P29/00,
            PC   A61P35/00,
            PC   A61P37/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12Q1/02,G01N33/15,G01N33/50,C12N15/00, PC
             A61K37/02,
            PC   C12N5/00
            CC   47 human secreted proteins
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:9606"
ORIGIN

  Query Match             90.1%;  Score 801.8;  DB 6;  Length 952;
  Best Local Similarity   98.2%;  Pred. No. 6.9e-217;
  Matches  842;  Conservative    0;  Mismatches   12;  Indels    3;  Gaps    3;

Qy         27 GGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCTCCCTGTGCTTAACCAGAGGTGC 86
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Db          1 GAATTCGGCACGAGGCCCTGGAAGCTGCCTGTCCTTCTCCCTGTGCTTAACCAGAGGTGC 60

Qy         87 CCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGGTGG 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGGTGG 120

Qy        147 TCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGGACA 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGGACA 180

Qy        207 CCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGG 266
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Db        181 CCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGG 240

Qy        267 TTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG-AGCCGATAGTC 325
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        241 TTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAAGCCGATAGTC 300

Qy        326 AAGTTCCCGGGGGGCCGTGGACGGCGCAACCTAT-ATCCTGGTGATGGTGGATCCAGATGC 384
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        301 AAGTTCCCGGGGGGCCGTGGACGGCGCAACCTATAATCCTGGTGATGGTGGATCCAGATGC 360

Qy        385 CCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAA 444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAA 420

Qy        445 GGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCC 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCC 480

Qy        505 CTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGG 564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGG 540

Qy        565 AAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAG 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAG 600

Qy        625 ATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAA 684
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAA 660

Qy        685 CTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC-A 743
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||| |
Db        661 CTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACAA 720

Qy        744 AAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCA 803
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Db        721 AAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCA 780

Qy        804 CACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTT 863
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTT 840

Qy        864 TCCAAATTAAAAAAAAA 880
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Db        841 TCCAAATAAAAAAAAAA 857


RESULT 11
BD139366
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LOCUS       BD139366                826 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Extended cDNA of secretory protein.
ACCESSION   BD139366
VERSION     BD139366.1  GI:23234311
KEYWORDS    JP 2002508182-A/118.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
  TITLE     Extended cDNA of secretory protein
  JOURNAL   Patent: JP 2002508182-A 118 19-MAR-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508182-A/118
            PD   19-MAR-2002
            PF   17-DEC-1998 JP 2000539136
            PR   17-DEC-1997 US    60/069957,09-FEB-1998 US    60/074121 PR
            13-APR-1998 US    60/081563,10-AUG-1998 US    60/096116 PI   LYDIE
            BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE  PI   EDWARDS
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
            Von Heijne matrix
            CC   score 8.5
            CC   seq AALLLGLMMVVTG/DE
            FH   Key             Location/Qualifiers
            FT   CDS             15. .695
            FT   sig_peptide     15. .80
            FT   polyA_signal    795. .800
            FT   polyA_site      814. .826.
FEATURES             Location/Qualifiers
     source          1. .826
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           88.1%;  Score 783.8;  DB 6;  Length 826;
  Best Local Similarity   99.0%;  Pred. No. 9.2e-212;
  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 60

Qy         135 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCT 194
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCC 120

Qy         195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
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Db         121 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 180

Qy         255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 240

Qy         315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 300

Qy         375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 360

Qy         435 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 494
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Db         361 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 420

Qy         495 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 554
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Db         421 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 480

Qy         555 TTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 614
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Db         481 TTCAGGAAGGAAAGGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 540

Qy         615 AAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 674
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Db         541 AAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 600

Qy         675 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGC 734
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Db         601 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGC 660

Qy         735 CCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 793
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Db         661 CCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 720

Qy         794 CATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 853
               |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         721 CATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 780

Qy         854 CCCCTTCTTTTCCAAATTAAAAAAAAA 880
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Db         781 CCCCTTCTTTTCCAAATAAAAAAAAA 807


RESULT 12
BD203800
LOCUS       BD203800                826 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  5'EST and human protein encoded thereby.
ACCESSION   BD203800
VERSION     BD203800.1  GI:33013570
KEYWORDS    JP 2002511259-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   Edwards,J.B.D.M., Duclert,A. and Giordano,J.Y.
  TITLE     5'EST and human protein encoded thereby
  JOURNAL   Patent: JP 2002511259-A 4 16-APR-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002511259-A/4
            PD   16-APR-2002
            PF   09-APR-1999 JP 2000543599
            PR   09-APR-1998 US    09/057719,28-APR-1998 US    09/069047 PI
            JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,JEAN YVES  PI
            GIORDANO
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12M1/00,C12N1/15, PC
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            PC   C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,G01N33/566, PC
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  Best Local Similarity   99.0%;  Pred. No. 9.2e-212;
  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
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Db          1 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 60

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Db         61 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCC 120

Qy        195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
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Db        121 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 180

Qy        255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
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Db        181 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 240

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
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Db        241 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 300

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
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Db        301 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 360

Qy        435 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 420

Qy        495 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 480

Qy        555 TTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 614
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Db        481 TTCAGGAAGGAAAGGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 540

Qy        615 AAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 674
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Qy        675 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGC 734
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Qy        735 CCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 793
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Qy        794 CATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 853
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Db        721 CATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 780

Qy        854 CCCCTTCTTTTCCAAATTAAAAAAAAA 880
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Db        781 CCCCTTCTTTTCCAAATAAAAAAAAA 807
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RESULT 13
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LOCUS       AR412374                826 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6639063.
ACCESSION   AR412374
VERSION     AR412374.1  GI:40167484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE     EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 7 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .826
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ORIGIN

  Query Match           88.1%;  Score 783.8;  DB 6;  Length 826;
  Best Local Similarity   99.0%;  Pred. No. 9.2e-212;
  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy         75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        135 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCT 194
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Db         61 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCC 120

Qy        195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
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Qy        255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
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Db        181 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 240

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
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Db        241 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 300

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 360

Qy        435 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 494
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Db        361 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 420

Qy        495 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 480

Qy        555 TTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 614
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Qy        615 AAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 674
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Qy        794 CATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 853
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Db        721 CATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 780

Qy        854 CCCCTTCTTTTCCAAATTAAAAAAAAA 880
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Db        781 CCCCTTCTTTTCCAAATAAAAAAAAA 807
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RESULT 14
AX884144
LOCUS       AX884144                826 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from Patent EP1033401.
ACCESSION   AX884144
VERSION     AX884144.1  GI:40039028
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  TITLE     Expressed sequence tags and encoded human proteins
  JOURNAL   Patent: EP 1033401-A 7 06-SEP-2000;
            Genset (FR)
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  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
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Db          61 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCC 120

Qy         195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
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Db         781 CCCCTTCTTTTCCAAATAAAAAAAAA 807


RESULT 15
AX969204
LOCUS       AX969204                826 bp    DNA     linear   PAT 15-JAN-2004
DEFINITION  Sequence 7 from Patent EP1104808.
ACCESSION   AX969204
VERSION     AX969204.1  GI:40975344
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
  TITLE     ESTs and encoded human proteins
  JOURNAL   Patent: EP 1104808-A 7 06-JUN-2001;
            Genset (FR)
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ORIGIN

  Query Match             88.1%;  Score 783.8;  DB 6;  Length 826;
  Best Local Similarity   99.0%;  Pred. No. 9.2e-212;
  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description

RESULT 1
ID AAA96350 standard; cDNA; 890 BP.
DE cDNA encoding a novel polypeptide designated PRO4408.
PN WO200056889-A2.
PD 28-SEP-2000.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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ID ABK33651 standard; cDNA; 890 BP.
DE cDNA encoding human PRO protein, Seq ID No 231.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 6; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 3
ID ABL88224 standard; cDNA; 890 BP.
DE Human PRO4408 cDNA sequence SEQ ID NO:305.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 4
ID ABL95713 standard; cDNA; 890 BP.
DE Human angiogenesis related cDNA PRO4408 SEQ ID NO: 305.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
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PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PN US2003008348-A1.
PD 09-JAN-2003.
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PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
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PN US2002192751-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
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PD 20-FEB-2003.
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PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
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PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
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PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
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PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
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PD 03-APR-2003.
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DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
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PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
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PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
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PN US2003092886-A1.
PD 15-MAY-2003.
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PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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ID ADB83967 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 25
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PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
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PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 28
ID ADC21950 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
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PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
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DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 35
ID ADC78178 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 36
ID ADD06413 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 37
ID ADD10594 standard; cDNA; 890 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #153.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 38
ID ADC77932 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 39
ID ADD11554 standard; cDNA; 890 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #153.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 40
ID ADD50895 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 41
ID ADD51141 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 42
ID ADD37347 standard; cDNA; 890 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #153.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 43
ID ADD50622 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 44
ID ADD50376 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 45
ID ADD51387 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 46
ID ACA06170 standard; cDNA; 890 BP.
DE cDNA encoding human PRO polypeptide #15.
PN US2003032061-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 47
ID ACA66956 standard; cDNA; 890 BP.
DE cDNA encoding human PRO polypeptide #116.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 48
ID ACD68708 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 10; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 49
ID ADC48934 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003092888-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 50
ID ADE21105 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 51
ID ADE05949 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 52
ID ADD75178 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 53
ID ADD75924 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 54
ID ADD85156 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 55
ID ADD86982 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 56
ID ADE20859 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 57
ID ADE39156 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 58
ID ADE05703 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 59
ID ADD73688 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 60
ID ADD78528 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 61
ID ADE41555 standard; cDNA; 890 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #153.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 62
ID ADE21351 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 63
ID ADD77466 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 64
ID ADE20613 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 65
ID ADD75678 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 66
ID ADD74194 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 67
ID ADD74440 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 68
ID ADD76170 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 69
ID ADD85662 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 70
ID ADE05211 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 71
ID ADD75424 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 72
ID ADD76968 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 73
ID ADD86736 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 74
ID ADD78204 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 75
ID ADD77712 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 76
ID ADD77958 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 77
ID ADD85416 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 78
ID ADD73948 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 79
ID ADD74686 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 80
ID ADD77214 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 81
ID ADD85908 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 82
ID ADE05457 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 83
ID ADD74932 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 84
ID ADG05744 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 85
ID ADG27298 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;

RESULT 86
ID ADG11361 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 87
ID ADG12140 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 88
ID ADF94697 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 89
ID ADG06793 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 90
ID ADH39137 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 91
ID ADH43738 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #153.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 92
ID ADG34227 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 93
ID ADI33697 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 94
ID ADH69791 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 95
ID ADI29952 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 96
ID ADM27349 standard; cDNA; 890 BP.
DE Novel human secreted and transmembrane protein PRO4408 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 97
ID ADK83083 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #153.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 98
ID ADK66707 standard; cDNA; 890 BP.
DE Human PRO polynucleotide #116.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 890; DB 12; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
RESULT 99
ID ADF09259 standard; cDNA; 889 BP.
DE Human secreted and transmembrane protein PRO4408 cDNA.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 98.7%; Score 878; DB 12; Length 889;
Best Local Similarity 99.9%; Pred. No. 7.2e-263;
RESULT 100
ID AAS22443 standard; cDNA; 972 BP.
DE Human cDNA encoding a novel human protein #9.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 98.3%; Score 874.8; DB 4; Length 972;
Best Local Similarity 99.8%; Pred. No. 7.5e-262;
RESULT 101
ID AAC77539 standard; cDNA; 909 BP.
DE Human ORFX ORF3094 polynucleotide sequence SEQ ID NO:6187.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 97.2%; Score 865.2; DB 3; Length 909;
Best Local Similarity 99.0%; Pred. No. 7.2e-259;
RESULT 102
ID AAC84882 standard; cDNA; 932 BP.
DE Human SEC1 nucleic acid sequence (clone ID 3445452).
PN WO200078802-A2.
PD 28-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match 97.2%; Score 865.2; DB 4; Length 932;
Best Local Similarity 99.0%; Pred. No. 7.3e-259;
RESULT 103
ID ADG76144 standard; cDNA; 932 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 57).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 97.2%; Score 865.2; DB 10; Length 932;
Best Local Similarity 99.0%; Pred. No. 7.3e-259;
RESULT 104
ID AAA15582 standard; cDNA; 903 BP.

DE Human phospholipid binding protein 2, PLBP2 gene.
PN US6063767-A.
PD 16-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 96.4%; Score 858.4; DB 3; Length 903;
Best Local Similarity 99.2%; Pred. No. 9.5e-257;
RESULT 105
ID ADK70378 standard; cDNA; 903 BP.
DE Respiratory disease differentially expressed cDNA #114.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 96.4%; Score 858.4; DB 12; Length 903;
Best Local Similarity 99.2%; Pred. No. 9.5e-257;
RESULT 106
ID AAF94490 standard; cDNA; 897 BP.
DE Human hydrophobic domain containing protein clone HP03880 cDNA #114.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 96.4%; Score 857.8; DB 4; Length 897;
Best Local Similarity 99.1%; Pred. No. 1.5e-256;
RESULT 107
ID ADB89000 standard; cDNA; 903 BP.
DE Human cDNA encoding Phospholipid binding protein, PLBP2.
PN US2003119730-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 96.1%; Score 855.2; DB 10; Length 903;
Best Local Similarity 99.0%; Pred. No. 9.5e-256;
RESULT 108
ID ADG76162 standard; cDNA; 879 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 75).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.8%; Score 835.2; DB 10; Length 879;
Best Local Similarity 99.0%; Pred. No. 1.6e-249;
RESULT 109
ID AAA78426 standard; cDNA; 1028 BP.
DE Human secreted protein gene 46 SEQ ID NO:56.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 833.2; DB 3; Length 1028;
Best Local Similarity 99.0%; Pred. No. 7.4e-249;
RESULT 110
ID ADK68203 standard; DNA; 876 BP.
DE Novel NOVX gene #65.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.6%; Score 832.8; DB 10; Length 876;
Best Local Similarity 99.1%; Pred. No. 9.1e-249;
RESULT 111
ID ADK68201 standard; DNA; 876 BP.
DE Novel NOVX gene #64.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.6%; Score 832.8; DB 10; Length 876;
Best Local Similarity 99.1%; Pred. No. 9.1e-249;
RESULT 112
ID ADK68181 standard; DNA; 876 BP.
DE Novel NOVX gene #54.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.4%; Score 831.2; DB 10; Length 876;
Best Local Similarity 98.9%; Pred. No. 2.9e-248;
RESULT 113
ID ADK68195 standard; DNA; 876 BP.
DE Novel NOVX gene #61.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.2%; Score 829.6; DB 10; Length 876;
Best Local Similarity 98.8%; Pred. No. 9.1e-248;
RESULT 114
ID ADK68197 standard; DNA; 876 BP.
DE Novel NOVX gene #62.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.2%; Score 829.6; DB 10; Length 876;
Best Local Similarity 98.8%; Pred. No. 9.1e-248;
RESULT 115
ID ADK68199 standard; DNA; 876 BP.
DE Novel NOVX gene #63.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.2%; Score 829.6; DB 10; Length 876;
Best Local Similarity 98.8%; Pred. No. 9.1e-248;
RESULT 116
ID ADK68191 standard; DNA; 876 BP.
DE Novel NOVX gene #59.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.2%; Score 829.6; DB 10; Length 876;
Best Local Similarity 98.8%; Pred. No. 9.1e-248;
RESULT 117
ID ADK68193 standard; DNA; 876 BP.
DE Novel NOVX gene #60.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 93.2%; Score 829.6; DB 10; Length 876;
Best Local Similarity 98.8%; Pred. No. 9.1e-248;
RESULT 118
ID ADR49184 standard; cDNA; 876 BP.
DE Human NOV8h cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 93.2%; Score 829.6; DB 13; Length 876;

Best Local Similarity 98.8%; Pred. No. 9.1e-248;
RESULT 119
ID ADR49180 standard; cDNA; 876 BP.
DE Human NOV8f cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 93.0%; Score 828; DB 13; Length 876;
Best Local Similarity 98.7%; Pred. No. 2.9e-247;
RESULT 120
ID ADR49182 standard; cDNA; 876 BP.
DE Human NOV8g cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 93.0%; Score 828; DB 13; Length 876;
Best Local Similarity 98.7%; Pred. No. 2.9e-247;
RESULT 121
ID ADR49192 standard; cDNA; 876 BP.
DE Human NOV8l cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 92.9%; Score 826.4; DB 13; Length 876;
Best Local Similarity 98.6%; Pred. No. 9e-247;
RESULT 122
ID ADR49170 standard; cDNA; 876 BP.
DE Human NOV8a cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 92.7%; Score 824.8; DB 13; Length 876;
Best Local Similarity 98.5%; Pred. No. 2.8e-246;
RESULT 123

ID ADR49186 standard; cDNA; 876 BP.
DE Human NOV8i cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 92.5%; Score 823.2; DB 13; Length 876;
Best Local Similarity 98.4%; Pred. No. 9e-246;
RESULT 124
ID ADR49188 standard; cDNA; 876 BP.
DE Human NOV8j cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 92.3%; Score 821.6; DB 13; Length 876;
Best Local Similarity 98.2%; Pred. No. 2.8e-245;
RESULT 125
ID AAA78431 standard; cDNA; 952 BP.
DE Human secreted protein gene 46 SEQ ID NO:61.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 90.1%; Score 801.8; DB 3; Length 952;
Best Local Similarity 98.2%; Pred. No. 4.5e-239;
RESULT 126
ID AAS22679 standard; cDNA; 886 BP.
DE Human cDNA encoding a novel human protein #245.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 88.2%; Score 785.4; DB 4; Length 886;
Best Local Similarity 98.6%; Pred. No. 5.6e-234;
RESULT 127
ID AAX97660 standard; DNA; 826 BP.
DE Extended human secreted protein coding sequence, SEQ ID NO. 124.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 88.1%; Score 783.8; DB 2; Length 826;
Best Local Similarity 99.0%; Pred. No. 1.7e-233;
RESULT 128
ID AAZ42252 standard; cDNA; 826 BP.
DE Human phosphatidylethanolamine-binding protein encoding cDNA.
PN WO9953051-A2.
PD 21-OCT-1999.
PA (GEST) GENSET.
Query Match 88.1%; Score 783.8; DB 3; Length 826;
Best Local Similarity 99.0%; Pred. No. 1.7e-233;
RESULT 129
ID AAC00013 standard; cDNA; 826 BP.
DE Human secreted protein cDNA sequence #4.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 88.1%; Score 783.8; DB 3; Length 826;
Best Local Similarity 99.0%; Pred. No. 1.7e-233;
RESULT 130
ID ADP18927 standard; cDNA; 826 BP.
DE Human secreted polynucleotide #183.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 88.1%; Score 783.8; DB 12; Length 826;
Best Local Similarity 99.0%; Pred. No. 1.7e-233;
RESULT 131
ID ADR49190 standard; cDNA; 808 BP.
DE Human NOV8k cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.

PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 77.0%; Score 685.2; DB 13; Length 808;
Best Local Similarity 91.0%; Pred. No. 9.9e-203;
RESULT 132
ID ADG76148 standard; cDNA; 706 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 61).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 74.9%; Score 666.2; DB 10; Length 706;
Best Local Similarity 99.4%; Pred. No. 7.8e-197;
RESULT 133
ID ADG76146 standard; cDNA; 706 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 59).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 74.7%; Score 664.6; DB 10; Length 706;
Best Local Similarity 99.3%; Pred. No. 2.5e-196;
RESULT 134
ID AAF94480 standard; cDNA; 681 BP.
DE Human hydrophobic domain containing protein clone HP03880 cDNA #104.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 74.6%; Score 664.2; DB 4; Length 681;
Best Local Similarity 99.4%; Pred. No. 3.2e-196;
RESULT 135
ID ACH04204 standard; cDNA; 615 BP.
DE Human cDNA differentially expressed in lung cancer #409.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Query Match 68.6%; Score 610.2; DB 9; Length 615;
Best Local Similarity 99.5%; Pred. No. 2.2e-179;
RESULT 136
ID ADG76164 standard; cDNA; 615 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 77).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 67.2%; Score 598.2; DB 10; Length 615;
Best Local Similarity 99.3%; Pred. No. 1.2e-175;
RESULT 137
ID ADK68187 standard; DNA; 627 BP.
DE Novel NOVX gene #57.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 67.2%; Score 598.2; DB 10; Length 627;
Best Local Similarity 99.3%; Pred. No. 1.2e-175;
RESULT 138
ID ADG76156 standard; cDNA; 634 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 69).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 67.2%; Score 598.2; DB 10; Length 634;
Best Local Similarity 99.3%; Pred. No. 1.2e-175;
RESULT 139
ID ADK68183 standard; DNA; 627 BP.
DE Novel NOVX gene #55.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 67.0%; Score 596.6; DB 10; Length 627;
Best Local Similarity 99.2%; Pred. No. 3.8e-175;
RESULT 140
ID ADR49176 standard; cDNA; 627 BP.
DE Human NOV8d cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 67.0%; Score 596.6; DB 13; Length 627;
Best Local Similarity 99.2%; Pred. No. 3.8e-175;
RESULT 141
ID ADR49172 standard; cDNA; 627 BP.
DE Human NOV8b cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 67.0%; Score 596.6; DB 13; Length 627;
Best Local Similarity 99.2%; Pred. No. 3.8e-175;

RESULT 142
ID ADG76154 standard; cDNA; 634 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 67).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 67.0%; Score 596.6; DB 10; Length 634;
Best Local Similarity 99.2%; Pred. No. 3.9e-175;
RESULT 143
ID ADG76152 standard; cDNA; 619 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 65).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 66.9%; Score 595.6; DB 10; Length 619;
Best Local Similarity 99.3%; Pred. No. 7.8e-175;
RESULT 144
ID ADK68189 standard; DNA; 627 BP.
DE Novel NOVX gene #58.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 66.7%; Score 593.4; DB 10; Length 627;
Best Local Similarity 98.9%; Pred. No. 3.8e-174;
RESULT 145
ID ADK68185 standard; DNA; 627 BP.
DE Novel NOVX gene #56.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 66.7%; Score 593.4; DB 10; Length 627;
Best Local Similarity 98.9%; Pred. No. 3.8e-174;
RESULT 146
ID ADR49174 standard; cDNA; 627 BP.
DE Human NOV8c cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 66.7%; Score 593.4; DB 13; Length 627;
Best Local Similarity 98.9%; Pred. No. 3.8e-174;
RESULT 147
ID ADG76150 standard; cDNA; 619 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 63).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 66.6%; Score 592.4; DB 10; Length 619;
Best Local Similarity 99.0%; Pred. No. 7.8e-174;
RESULT 148
ID ADR49178 standard; cDNA; 627 BP.
DE Human NOV8e cDNA.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 66.5%; Score 591.8; DB 13; Length 627;
Best Local Similarity 98.7%; Pred. No. 1.2e-173;
RESULT 149
ID ADG76158 standard; cDNA; 547 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 71).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 59.3%; Score 527.6; DB 10; Length 547;
Best Local Similarity 99.3%; Pred. No. 1.2e-153;
RESULT 150
ID ADG76160 standard; cDNA; 547 BP.
DE Human NOVX cDNA to treat human pathological conditions (SeqID 73).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 59.1%; Score 526; DB 10; Length 547;
Best Local Similarity 99.1%; Pred. No. 3.8e-153;
RESULT 151
ID AAX40582 standard; cDNA; 447 BP.
DE Human secreted protein 5' EST SEQ ID No: 182.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 48.7%; Score 433; DB 2; Length 447;
Best Local Similarity 98.9%; Pred. No. 3.6e-124;
RESULT 152
ID ADQ51836 standard; DNA; 591 BP.
DE Novel canine microarray-related DNA sequence SeqID3138.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 42.4%; Score 377.8; DB 13; Length 591;
Best Local Similarity 78.2%; Pred. No. 7e-107;
RESULT 153

ID ACH18647 standard; cDNA; 429 BP.
DE Human adult heart cDNA #2961.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 33.4%; Score 297.2; DB 9; Length 429;
Best Local Similarity 95.9%; Pred. No. 8.3e-82;
RESULT 154
ID AAD56351 standard; DNA; 1227 BP.
DE Human secreted protein-encoding gene 1 cDNA clone HNMIK76, SEQ ID NO:11.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.3%; Score 207; DB 9; Length 1227;
Best Local Similarity 99.0%; Pred. No. 2.1e-53;
RESULT 155
ID AAS62175 standard; cDNA; 303 BP.
DE Porcine muscular steatosis-modulating factor #301.
PN WO200179287-A2.
PD 25-OCT-2001.
PA (MIAC) CANADA AGRIC & AGRI-FOOD CANADA.
Query Match 18.4%; Score 164.2; DB 6; Length 303;
Best Local Similarity 80.1%; Pred. No. 2.2e-40;
RESULT 156
ID AAH85783 standard; DNA; 133 BP.
DE Human single nucleotide polymorphism containing DNA sequence #640.
PN WO9953095-A2.
PD 21-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 13.5%; Score 120.2; DB 2; Length 133;
Best Local Similarity 96.8%; Pred. No. 7.6e-27;
RESULT 157
ID AAD42243 standard; cDNA; 1191 BP.
DE Corn FT homologue cDNA from clone p0081.chcad07r.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.4%; Score 48.2; DB 6; Length 1191;
Best Local Similarity 60.2%; Pred. No. 0.00072;
RESULT 158
ID ADR04250 standard; cDNA; 1191 BP.
DE Corn FT homologue encoding cDNA SEQ ID NO:17.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.4%; Score 48.2; DB 13; Length 1191;
Best Local Similarity 60.2%; Pred. No. 0.00072;
RESULT 159
ID AAD42238 standard; cDNA; 1078 BP.
DE Corn FT homologue cDNA #1.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.3%; Score 47.2; DB 6; Length 1078;
Best Local Similarity 59.8%; Pred. No. 0.0014;
RESULT 160
ID ADR04240 standard; cDNA; 1078 BP.
DE Corn FT homologue encoding cDNA SEQ ID NO:7.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.3%; Score 47.2; DB 13; Length 1078;
Best Local Similarity 59.8%; Pred. No. 0.0014;
RESULT 161
ID ABT09032 standard; DNA; 686 BP.
DE Phase-1 Rat CT gene SEQ ID No 120.
PN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 5.3%; Score 47; DB 6; Length 686;
Best Local Similarity 45.7%; Pred. No. 0.0013;
RESULT 162
ID ADG45730 standard; DNA; 686 BP.
DE Liver inflammatory predictive gene related DNA sequence.
PN WO2003095624-A2.
PD 20-NOV-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 5.3%; Score 47; DB 12; Length 686;
Best Local Similarity 45.7%; Pred. No. 0.0013;
RESULT 163
ID ADH22989 standard; DNA; 686 BP.
DE Partial DNA seqeunce of a rat kidney toxicity predictive gene (317).
PN WO2003100030-A2.
PD 04-DEC-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 5.3%; Score 47; DB 12; Length 686;
Best Local Similarity 45.7%; Pred. No. 0.0013;
RESULT 164
ID ADR91301 standard; cDNA; 686 BP.
DE Spleen necrosis predictive cDNA sequence, SEQ ID No 257.
PN WO2004083402-A2.
PD 30-SEP-2004.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 5.3%; Score 47; DB 13; Length 686;
Best Local Similarity 45.7%; Pred. No. 0.0013;
RESULT 165
ID ADF30543 standard; cDNA; 1037 BP.
DE Rat angiogenesis modulating protein cDNA #26.
PN US2003162706-A1.
PD 28-AUG-2003.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 5.3%; Score 47; DB 10; Length 1037;
Best Local Similarity 45.7%; Pred. No. 0.0016;
RESULT 166
ID AAQ30001 standard; cDNA to mRNA; 1047 BP.
DE HCNP precursor gene #1.
PN EP511816-A2.
PD 04-NOV-1992.
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (OJIK/) OJIKA K.
PA (YAMA/) YAMAMOTO M.
Query Match 5.3%; Score 47; DB 2; Length 1047;
Best Local Similarity 45.7%; Pred. No. 0.0016;
RESULT 167
ID AAQ58685 standard; cDNA to mRNA; 1047 BP.
DE Rat hippocampal cholinergic neurotrophic peptide precursor cDNA.
PN WO9405788-A1.
PD 17-MAR-1994.
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (YAMA/) YAMAMOTO M.
Query Match 5.3%; Score 47; DB 2; Length 1047;
Best Local Similarity 45.7%; Pred. No. 0.0016;
RESULT 168
ID ADB58289 standard; DNA; 1075 BP.
DE Toxicity-related gene, SEQ ID 3315.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 5.3%; Score 47; DB 10; Length 1075;
Best Local Similarity 45.7%; Pred. No. 0.0016;
RESULT 169
ID ADB52831 standard; DNA; 1075 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3373.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 5.3%; Score 47; DB 10; Length 1075;
Best Local Similarity 45.7%; Pred. No. 0.0016;
RESULT 170
ID ADF30541 standard; cDNA; 1075 BP.

DE Rat angiogenesis modulating protein cDNA #25.
PN US2003162706-A1.
PD 28-AUG-2003.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 5.3%; Score 47; DB 10; Length 1075;
Best Local Similarity 45.7%; Pred. No. 0.0016;
RESULT 171
ID ADP72991 standard; DNA; 1075 BP.
DE Renal toxin progression gene marker #1580.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 5.3%; Score 47; DB 12; Length 1075;
Best Local Similarity 45.7%; Pred. No. 0.0016;
RESULT 172
ID AAD42256 standard; cDNA; 886 BP.
DE Wheat FT homologue cDNA from clone wdk9n1.pk001.o20.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.2%; Score 46.2; DB 6; Length 886;
Best Local Similarity 59.5%; Pred. No. 0.0026;
RESULT 173
ID ADR04276 standard; cDNA; 886 BP.
DE Wheat FT homologue encoding cDNA SEQ ID NO:43.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.2%; Score 46.2; DB 13; Length 886;
Best Local Similarity 59.5%; Pred. No. 0.0026;
RESULT 174
ID ABK91072 standard; DNA; 847 BP.
DE Rice Hd3a gene associated DNA sequence #2.
PN WO200242475-A1.
PD 30-MAY-2002.
PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
Query Match 5.1%; Score 45.4; DB 6; Length 847;
Best Local Similarity 59.8%; Pred. No. 0.0045;
RESULT 175
ID ABK91071 standard; DNA; 847 BP.
DE Rice Hd3a gene associated DNA sequence #1.
PN WO200242475-A1.
PD 30-MAY-2002.
PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
Query Match 5.1%; Score 45.4; DB 6; Length 847;
Best Local Similarity 59.8%; Pred. No. 0.0045;
RESULT 176
ID ABL19451 standard; DNA; 770 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9826.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 43.2; DB 4; Length 770;
Best Local Similarity 50.5%; Pred. No. 0.021;
RESULT 177
ID ABL02286 standard; cDNA; 2654 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 1340.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 43.2; DB 4; Length 2654;
Best Local Similarity 50.5%; Pred. No. 0.04;
RESULT 178
ID ABL19450 standard; DNA; 3051 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9823.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 43.2; DB 4; Length 3051;
Best Local Similarity 50.5%; Pred. No. 0.043;

RESULT 179
ID ABX47739 standard; cDNA; 398 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12904.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 42.8; DB 8; Length 398;
Best Local Similarity 60.2%; Pred. No. 0.019;
RESULT 180
ID ABX44623 standard; cDNA; 425 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9788.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 42.8; DB 8; Length 425;
Best Local Similarity 60.2%; Pred. No. 0.02;
RESULT 181
ID ABX46766 standard; cDNA; 441 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11931.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 42.8; DB 8; Length 441;
Best Local Similarity 60.2%; Pred. No. 0.02;
RESULT 182
ID ABX36953 standard; cDNA; 459 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2118.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 42.8; DB 8; Length 459;
Best Local Similarity 60.2%; Pred. No. 0.021;
RESULT 183
ID ABL16352 standard; DNA; 2730 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 529.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 42.8; DB 4; Length 2730;
Best Local Similarity 52.9%; Pred. No. 0.054;
RESULT 184
ID ADL33431 standard; cDNA; 842 BP.
DE Festuca arundinacea floral development protein cDNA SEQ ID NO:6.
PN WO2004022755-A2.
PD 18-MAR-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Query Match 4.7%; Score 42.2; DB 12; Length 842;
Best Local Similarity 58.3%; Pred. No. 0.045;
RESULT 185
ID ACH16028 standard; cDNA; 428 BP.
DE Human adult heart cDNA #342.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.6%; Score 41; DB 9; Length 428;
Best Local Similarity 60.2%; Pred. No. 0.073;

RESULT 186
ID ACH30218 standard; cDNA; 431 BP.
DE Human testis cDNA #604.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.6%; Score 41; DB 9; Length 431;
Best Local Similarity 60.2%; Pred. No. 0.074;
RESULT 187
ID ACH43544 standard; cDNA; 474 BP.
DE Human foetal brain cDNA #4269.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.6%; Score 41; DB 9; Length 474;
Best Local Similarity 60.2%; Pred. No. 0.078;
RESULT 188
ID ACH45066 standard; cDNA; 485 BP.
DE Human foetal brain cDNA #5791.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.6%; Score 41; DB 9; Length 485;
Best Local Similarity 60.2%; Pred. No. 0.078;
RESULT 189
ID ACH40483 standard; cDNA; 486 BP.
DE Human foetal brain cDNA #1850.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.6%; Score 41; DB 9; Length 486;
Best Local Similarity 60.2%; Pred. No. 0.079;
RESULT 190
ID ABZ84647 standard; cDNA; 511 BP.
DE Toxicologically relevant human nucleotide sequence #1806.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 4.6%; Score 41; DB 10; Length 511;
Best Local Similarity 60.2%; Pred. No. 0.081;
RESULT 191
ID ACH39331 standard; cDNA; 576 BP.
DE Human foetal brain cDNA #698.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.6%; Score 41; DB 9; Length 576;
Best Local Similarity 60.2%; Pred. No. 0.086;
RESULT 192
ID ACD19363 standard; cDNA; 618 BP.
DE cDNA encoding novel human protein #43.
PN WO2003023002-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.6%; Score 41; DB 10; Length 618;
Best Local Similarity 60.2%; Pred. No. 0.089;
RESULT 193
ID AAD57645 standard; DNA; 831 BP.
DE Rice enhanced yield gene, FT.
PN WO2003048319-A2.
PD 12-JUN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.6%; Score 41; DB 10; Length 831;
Best Local Similarity 56.2%; Pred. No. 0.1;
RESULT 194
ID ABZ11578 standard; cDNA; 916 BP.
DE Human polynucleotide SEQ ID NO 460.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 41; DB 6; Length 916;
Best Local Similarity 60.2%; Pred. No. 0.11;
RESULT 195
ID ADM44096 standard; cDNA; 916 BP.
DE Novel human arginine-rich protein cDNA #460.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 4.6%; Score 41; DB 12; Length 916;
Best Local Similarity 60.2%; Pred. No. 0.11;
RESULT 196
ID AAQ80734 standard; cDNA to mRNA; 1001 BP.
DE Phosphatidylethanolamine binding protein coding sequence.
PN EP628631-A1.
PD 14-DEC-1994.
PA (ONOY) ONO PHARM CO LTD.
Query Match 4.6%; Score 41; DB 2; Length 1001;
Best Local Similarity 60.2%; Pred. No. 0.12;
RESULT 197
ID ABQ93324 standard; cDNA; 1079 BP.
DE Human cDNA SEQ ID NO 37.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 41; DB 6; Length 1079;
Best Local Similarity 60.2%; Pred. No. 0.12;
RESULT 198
ID ACD19364 standard; cDNA; 1434 BP.
DE cDNA encoding novel human protein #44.
PN WO2003023002-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.6%; Score 41; DB 10; Length 1434;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 199
ID ABK70296 standard; cDNA; 1444 BP.
DE Human lung cancer associated full length cDNA DMSM-99.
PN WO200224057-A2.
PD 28-MAR-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.6%; Score 41; DB 6; Length 1444;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 200
ID ABN97295 standard; DNA; 1444 BP.
DE Gene #3793 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.6%; Score 41; DB 6; Length 1444;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 201
ID ADH28747 standard; DNA; 1444 BP.
DE Human chronic myclogenous leukaemia (CML) gene marker #15.
PN US2003104426-A1.

PD 05-JUN-2003.
PA (LINS/) LINSLEY P S.
PA (MAOM/) MAO M.
PA (DAIH/) DAI H.
PA (HEYY/) HE Y.
PA (RADI/) RADICH J P.
Query Match 4.6%; Score 41; DB 10; Length 1444;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 202
ID ACN39579 standard; cDNA; 1444 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325783, SEQ ID NO:3816.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.6%; Score 41; DB 13; Length 1444;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 203
ID ADP23850 standard; cDNA; 1444 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1028.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.6%; Score 41; DB 13; Length 1444;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 204
ID AAQ30002 standard; cDNA to mRNA; 1447 BP.
DE HCNP precursor gene #2.
PN EP511816-A2.
PD 04-NOV-1992.
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (OJIK/) OJIKA K.
PA (YAMA/) YAMAMOTO M.
Query Match 4.6%; Score 41; DB 2; Length 1447;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 205
ID AAQ58686 standard; cDNA to mRNA; 1447 BP.
DE Human hippocampal cholinergic neurotrophic peptide precursor cDNA.
PN WO9405788-A1.
PD 17-MAR-1994.
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (YAMA/) YAMAMOTO M.
Query Match 4.6%; Score 41; DB 2; Length 1447;
Best Local Similarity 60.2%; Pred. No. 0.14;
RESULT 206
ID ABV29440 standard; cDNA; 1732 BP.
DE Human prostate expression marker cDNA 29431.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 41; DB 5; Length 1732;
Best Local Similarity 60.2%; Pred. No. 0.16;
RESULT 207
ID AAD42242 standard; cDNA; 837 BP.
DE Corn FT homologue cDNA from clone p0014.ctush42r.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 40.8; DB 6; Length 837;
Best Local Similarity 56.8%; Pred. No. 0.12;
RESULT 208
ID ADR04248 standard; cDNA; 837 BP.
DE Corn FT homologue encoding cDNA SEQ ID NO:15.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 40.8; DB 13; Length 837;
Best Local Similarity 56.8%; Pred. No. 0.12;
RESULT 209
ID ADK55916 standard; DNA; 599 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3299.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.6%; Score 40.6; DB 10; Length 599;
Best Local Similarity 62.1%; Pred. No. 0.12;
RESULT 210
ID ADK59561 standard; DNA; 610 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6944.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.6%; Score 40.6; DB 10; Length 610;
Best Local Similarity 62.1%; Pred. No. 0.12;
RESULT 211
ID ADC03460 standard; DNA; 1077 BP.
DE Wheat flowering time-related DNA sequence #20.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.6%; Score 40.6; DB 10; Length 1077;
Best Local Similarity 56.3%; Pred. No. 0.16;
RESULT 212
ID ADC03448 standard; DNA; 1077 BP.
DE Wheat flowering time-related DNA sequence #8.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.6%; Score 40.6; DB 10; Length 1077;
Best Local Similarity 56.3%; Pred. No. 0.16;
RESULT 213
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.6%; Score 40.6; DB 8; Length 2000;
Best Local Similarity 10.2%; Pred. No. 0.22;
RESULT 214
ID ADQ84782 standard; cDNA; 1312 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1596.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 4.5%; Score 40; DB 13; Length 1312;
Best Local Similarity 61.5%; Pred. No. 0.27;
RESULT 215
ID ABX39978 standard; cDNA; 424 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5143.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.4%; Score 39.6; DB 8; Length 424;
Best Local Similarity 58.5%; Pred. No. 0.2;
RESULT 216
ID AAC42966 standard; DNA; 528 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37529.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.4%; Score 39.6; DB 3; Length 528;
Best Local Similarity 54.9%; Pred. No. 0.22;
RESULT 217
ID ABZ14830 standard; DNA; 528 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2635.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.4%; Score 39.6; DB 6; Length 528;

Best Local Similarity 54.9%; Pred. No. 0.22;
RESULT 218
ID AAF82481 standard; cDNA; 561 BP.
DE Mouse pebp-2 cDNA.
PN WO200123424-A1.
PD 05-APR-2001.
PA (MONU) UNIV MONASH.
Query Match 4.4%; Score 39.4; DB 4; Length 561;
Best Local Similarity 51.4%; Pred. No. 0.27;
RESULT 219
ID AAF82483 standard; cDNA; 578 BP.
DE Mouse cDNA encoding pebp-2 21 kDa form.
PN WO200123424-A1.
PD 05-APR-2001.
PA (MONU) UNIV MONASH.
Query Match 4.4%; Score 39.4; DB 4; Length 578;
Best Local Similarity 51.4%; Pred. No. 0.27;
RESULT 220
ID AAF82492 standard; cDNA; 1218 BP.
DE Mouse pebp-2 cDNA.
PN WO200123424-A1.
PD 05-APR-2001.
PA (MONU) UNIV MONASH.
Query Match 4.4%; Score 39.4; DB 4; Length 1218;
Best Local Similarity 51.4%; Pred. No. 0.41;
RESULT 221
ID ABD04138 standard; DNA; 660 BP.
DE Pseudomonas aeruginosa polynucleotide #2742.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.4%; Score 39; DB 11; Length 660;
Best Local Similarity 47.1%; Pred. No. 0.39;
RESULT 222
ID ABD04423 standard; DNA; 768 BP.
DE Pseudomonas aeruginosa polynucleotide #3027.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.4%; Score 39; DB 11; Length 768;
Best Local Similarity 47.1%; Pred. No. 0.42;
RESULT 223
ID ABL10663 standard; cDNA; 974 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 26471.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 39; DB 4; Length 974;
Best Local Similarity 53.0%; Pred. No. 0.48;
RESULT 224
ID ABD04235 standard; DNA; 1671 BP.
DE Pseudomonas aeruginosa polynucleotide #2839.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.4%; Score 39; DB 11; Length 1671;
Best Local Similarity 47.1%; Pred. No. 0.64;
RESULT 225
ID ABD04523 standard; DNA; 2352 BP.
DE Pseudomonas aeruginosa polynucleotide #3127.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.4%; Score 39; DB 11; Length 2352;
Best Local Similarity 47.1%; Pred. No. 0.77;
RESULT 226
ID ABL27740 standard; DNA; 2621 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 34693.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 39; DB 4; Length 2621;
Best Local Similarity 53.0%; Pred. No. 0.82;
RESULT 227
ID ABL10662 standard; cDNA; 2974 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 26468.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 39; DB 4; Length 2974;
Best Local Similarity 53.0%; Pred. No. 0.87;
RESULT 228
ID ADO03797 standard; DNA; 189 BP.
DE Human Raf kinase inhibitor protein (RKIP) gene RKIP motif DNA.
PN US2004018570-A1.
PD 29-JAN-2004.
PA (UYBR-) UNIV BROWN.
Query Match 4.4%; Score 38.8; DB 12; Length 189;
Best Local Similarity 57.4%; Pred. No. 0.23;
RESULT 229
ID ADS18413 standard; DNA; 189 BP.
DE Human RKIP protein encoding gene.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 4.3%; Score 38.6; DB 13; Length 189;
Best Local Similarity 59.6%; Pred. No. 0.27;
RESULT 230
ID ABX52843 standard; cDNA; 358 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2772.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.3%; Score 38.4; DB 8; Length 358;
Best Local Similarity 57.5%; Pred. No. 0.43;
RESULT 231
ID AAA60684 standard; DNA; 528 BP.
DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:3.
PN JP2000139250-A.
PD 23-MAY-2000.
PA (TORA) TORAY IND INC.
Query Match 4.3%; Score 38; DB 3; Length 528;
Best Local Similarity 54.2%; Pred. No. 0.71;
RESULT 232
ID AAD42235 standard; cDNA; 492 BP.
DE Peruvian lily FT homologue cDNA from clone eallc.pk006.e6.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.2%; Score 37.8; DB 6; Length 492;
Best Local Similarity 54.7%; Pred. No. 0.79;
RESULT 233
ID ADR04234 standard; cDNA; 492 BP.
DE Peruvian lily FT homologue encoding cDNA SEQ ID NO:1.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.2%; Score 37.8; DB 13; Length 492;
Best Local Similarity 54.7%; Pred. No. 0.79;
RESULT 234
ID ADL33432 standard; cDNA; 825 BP.
DE Lolium perenne floral development protein cDNA SEQ ID NO:7.
PN WO2004022755-A2.
PD 18-MAR-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Query Match 4.2%; Score 37.8; DB 12; Length 825;
Best Local Similarity 58.4%; Pred. No. 1;
RESULT 235
ID ADN94934 standard; cDNA; 1017 BP.
DE Indian rice Kasalath variety flowering-related RFT1 cDNA.
PN JP2004089036-A.

PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 4.2%; Score 37.8; DB 12; Length 1017;
Best Local Similarity 54.7%; Pred. No. 1.2;
RESULT 236
ID ADN94937 standard; cDNA; 1037 BP.
DE Japanese rice Nipponbare variety flowering-related RFT1 cDNA.
PN JP2004089036-A.
PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 4.2%; Score 37.8; DB 12; Length 1037;
Best Local Similarity 54.7%; Pred. No. 1.2;
RESULT 237
ID ACA23809 standard; DNA; 1193 BP.
DE Prokaryotic essential gene #5466.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 37.8; DB 8; Length 1193;
Best Local Similarity 51.5%; Pred. No. 1.3;
RESULT 238
ID ABD33098 standard; DNA; 219352 BP.
DE Murine cancer-associated (CA) gene MD07-008.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.2%; Score 37.8; DB 13; Length 219352;
Best Local Similarity 51.5%; Pred. No. 21;
RESULT 239
ID ADE57791 standard; DNA; 1795 BP.
DE Rat gene M33648, SEQ ID NO 3656.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.2%; Score 37.4; DB 10; Length 1795;
Best Local Similarity 50.9%; Pred. No. 2.1;
RESULT 240
ID ADE57787 standard; DNA; 1795 BP.
DE Rat gene M33648, SEQ ID NO 3652.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.2%; Score 37.4; DB 10; Length 1795;
Best Local Similarity 50.9%; Pred. No. 2.1;
RESULT 241
ID ABL09411 standard; cDNA; 687 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22715.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.2%; Score 37.2; DB 4; Length 687;
Best Local Similarity 57.9%; Pred. No. 1.5;
RESULT 242
ID ABL09410 standard; cDNA; 2744 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22712.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.2%; Score 37.2; DB 4; Length 2744;
Best Local Similarity 57.9%; Pred. No. 3.1;
RESULT 243
ID AAA60683 standard; DNA; 528 BP.
DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:2.
PN JP2000139250-A.
PD 23-MAY-2000.
PA (TORA) TORAY IND INC.
Query Match 4.1%; Score 36.8; DB 3; Length 528;
Best Local Similarity 55.5%; Pred. No. 1.7;
RESULT 244
ID AAC48359 standard; DNA; 754 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57192.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 36.8; DB 3; Length 754;
Best Local Similarity 55.5%; Pred. No. 2;
RESULT 245
ID AAC34682 standard; DNA; 775 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7506.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 36.8; DB 3; Length 775;
Best Local Similarity 55.5%; Pred. No. 2.1;
RESULT 246
ID ADC77636 standard; cDNA; 831 BP.
DE A.thaliana flowering locus T (FT) cDNA.
PN US2003093835-A1.
PD 15-MAY-2003.
PA (WEIG/) WEIGEL D.
PA (AHNJ/) AHN J H.
Query Match 4.1%; Score 36.8; DB 10; Length 831;
Best Local Similarity 55.5%; Pred. No. 2.1;
RESULT 247
ID AAZ28491 standard; cDNA; 856 BP.
DE Flowering locus T (FT) gene antisense insert.
PN WO9953070-A1.
PD 21-OCT-1999.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 4.1%; Score 36.8; DB 2; Length 856;
Best Local Similarity 55.5%; Pred. No. 2.2;
RESULT 248
ID AAZ28490 standard; cDNA; 856 BP.
DE Flowering locus T (FT) gene.
PN WO9953070-A1.
PD 21-OCT-1999.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 4.1%; Score 36.8; DB 2; Length 856;
Best Local Similarity 55.5%; Pred. No. 2.2;
RESULT 249
ID ABK89245 standard; DNA; 1210 BP.
DE Mouse DNA for a nerve related protein.
PN JP2002176881-A.
PD 25-JUN-2002.
PA (OSHI/) OSHIKA Y.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 4.1%; Score 36.8; DB 6; Length 1210;
Best Local Similarity 44.5%; Pred. No. 2.6;
RESULT 250
ID ABZ52773 standard; cDNA; 600 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 1886.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORQ) NAT FOOD RES INST MIN AGRIC.
Query Match 4.1%; Score 36.4; DB 8; Length 600;
Best Local Similarity 48.5%; Pred. No. 2.4;
RESULT 251
ID AAF13966 standard; cDNA; 851 BP.
DE Aspergillus oryzae EST SEQ ID NO:6489.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Query Match 4.1%; Score 36.4; DB 3; Length 851;
Best Local Similarity 48.5%; Pred. No. 2.9;
RESULT 252
ID AAD42263 standard; cDNA; 1004 BP.
DE Rice FT homologue cDNA from clone rsr9n.pk001.d1:fis.
PN WO200244390-A2.
PD 06-JUN-2002.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.1%; Score 36.4; DB 6; Length 1004;
Best Local Similarity 64.0%; Pred. No. 3.2;
RESULT 253
ID ADR04292 standard; cDNA; 1004 BP.
DE Rice FT homologue encoding cDNA SEQ ID NO:59.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.1%; Score 36.4; DB 13; Length 1004;
Best Local Similarity 64.0%; Pred. No. 3.2;
RESULT 254
ID ADT42165 standard; cDNA; 1554 BP.
DE Bacterial polynucleotide #16916.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 36.4; DB 13; Length 1554;
Best Local Similarity 48.1%; Pred. No. 4;
RESULT 255
ID ACA90170 standard; cDNA; 732 BP.
DE cDNA encoding novel human protein NOV8a.
PN WO2003031571-A2.
PD 17-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 36.2; DB 8; Length 732;
Best Local Similarity 57.5%; Pred. No. 3.1;
RESULT 256
ID ADQ75720 standard; cDNA; 2718 BP.
DE Codon optimised hCMV gB coding sequence #1.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICA-) VICAL INC.
Query Match 4.0%; Score 36; DB 12; Length 2718;
Best Local Similarity 60.0%; Pred. No. 7.2;
RESULT 257
ID ADO09333 standard; cDNA; 732 BP.
DE Novel human protein Nov8a cDNA.
PN US2004014058-A1.
PD 22-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (CHAN/) CHANT J S.
PA (CHAU/) CHAUDHURI A.
PA (EDIN/) EDINGER S.
PA (GERL/) GERLACH V.
PA (GIOT/) GIOT L.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLET I.
PA (OOIC/) OOI C E.
PA (PATT/) PATTURAJAN M.
PA (RIEG/) RIEGER D K.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (ZERH/) ZERHUSEN B D.
PA (ZHON/) ZHONG H.
PA (ZHON/) ZHONG M.
Query Match 4.0%; Score 35.2; DB 12; Length 732;
Best Local Similarity 52.6%; Pred. No. 6.3;
RESULT 258
ID AAD42249 standard; cDNA; 1226 BP.
DE Rice FT homologue cDNA from clone rls24.pk0017.c7.
PN WO200244390-A2.
PD 06-JUN-2002.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.0%; Score 35.2; DB 6; Length 1226;
Best Local Similarity 47.2%; Pred. No. 8.3;
RESULT 259
ID ADR04262 standard; cDNA; 1226 BP.
DE Rice FT homologue encoding cDNA SEQ ID NO:29.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.0%; Score 35.2; DB 13; Length 1226;
Best Local Similarity 47.2%; Pred. No. 8.3;
RESULT 260
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.0%; Score 35.2; DB 8; Length 2000;
Best Local Similarity 8.3%; Pred. No. 11;
RESULT 261
ID AAS91643 standard; cDNA; 598 BP.
DE DNA encoding novel human diagnostic protein #27447.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 35; DB 5; Length 598;
Best Local Similarity 57.9%; Pred. No. 6.5;
RESULT 262
ID ABL09966 standard; cDNA; 5190 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 24380.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 35; DB 4; Length 5190;
Best Local Similarity 59.6%; Pred. No. 21;
RESULT 263
ID ADK56422 standard; DNA; 411 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3805.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.9%; Score 34.8; DB 10; Length 411;
Best Local Similarity 58.8%; Pred. No. 6.2;
RESULT 264
ID ADG33861 standard; DNA; 1383 BP.
DE Actinomycetes dual condensation/epimerisation NRPS domain DNA ID 120.
PN WO2003089641-A2.
PD 30-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.9%; Score 34.8; DB 10; Length 1383;
Best Local Similarity 53.7%; Pred. No. 12;
RESULT 265
ID ABX34790 standard; cDNA; 1652 BP.
DE Human mddt cDNA SEQ ID 351.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 34.8; DB 8; Length 1652;
Best Local Similarity 47.3%; Pred. No. 13;
RESULT 266
ID AAF82482 standard; cDNA; 539 BP.
DE Mouse cDNA encoding pebp-2 20 kDa form.
PN WO200123424-A1.
PD 05-APR-2001.
PA (MONU) UNIV MONASH.
Query Match 3.9%; Score 34.6; DB 4; Length 539;
Best Local Similarity 56.6%; Pred. No. 8.3;
RESULT 267
ID ADT45701 standard; cDNA; 1482 BP.
DE Bacterial polynucleotide #20452.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.9%; Score 34.6; DB 13; Length 1482;
Best Local Similarity 52.4%; Pred. No. 14;
RESULT 268
ID ADH10487 standard; DNA; 1560 BP.
DE Human cancer-related polynucleotide, SEQ ID 9.
PN WO2003106627-A2.
PD 24-DEC-2003.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 34.6; DB 12; Length 1560;
Best Local Similarity 53.0%; Pred. No. 15;
RESULT 269
ID ADH10489 standard; DNA; 1691 BP.
DE Human cancer-related polynucleotide, SEQ ID 11.
PN WO2003106627-A2.
PD 24-DEC-2003.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 34.6; DB 12; Length 1691;
Best Local Similarity 53.0%; Pred. No. 15;
RESULT 270
ID ADH10480 standard; DNA; 1703 BP.
DE Human cancer-related polynucleotide, SEQ ID 2.
PN WO2003106627-A2.
PD 24-DEC-2003.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 34.6; DB 12; Length 1703;
Best Local Similarity 53.0%; Pred. No. 15;
RESULT 271
ID ADH10483 standard; DNA; 1745 BP.
DE Human cancer-related polynucleotide, SEQ ID 5.
PN WO2003106627-A2.
PD 24-DEC-2003.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 34.6; DB 12; Length 1745;
Best Local Similarity 53.0%; Pred. No. 15;
RESULT 272
ID ADH10479 standard; DNA; 1764 BP.
DE Human cancer-related polynucleotide, SEQ ID 1.
PN WO2003106627-A2.
PD 24-DEC-2003.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 34.6; DB 12; Length 1764;
Best Local Similarity 53.0%; Pred. No. 16;
RESULT 273
ID ADH10485 standard; DNA; 1871 BP.
DE Human cancer-related polynucleotide, SEQ ID 7.
PN WO2003106627-A2.
PD 24-DEC-2003.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 34.6; DB 12; Length 1871;
Best Local Similarity 53.0%; Pred. No. 16;
RESULT 274
ID ADH10482 standard; DNA; 1890 BP.
DE Human cancer-related polynucleotide, SEQ ID 4.
PN WO2003106627-A2.
PD 24-DEC-2003.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 34.6; DB 12; Length 1890;
Best Local Similarity 53.0%; Pred. No. 16;
RESULT 275
ID ABK15038 standard; cDNA; 15690 BP.
DE Canine distemper virus cDNA.
PN WO200200883-A2.
PD 03-JAN-2002.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 3.9%; Score 34.6; DB 6; Length 15690;
Best Local Similarity 54.3%; Pred. No. 50;
RESULT 276
ID ABK15000 standard; DNA; 15690 BP.
DE Canine distemper virus positive, antigenomic strand.
PN WO200200883-A2.
PD 03-JAN-2002.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 3.9%; Score 34.6; DB 6; Length 15690;
Best Local Similarity 54.3%; Pred. No. 50;
RESULT 277
ID ABK15039 standard; DNA; 18826 BP.
DE Canine distemper virus full length genomic clone plus vector.
PN WO200200883-A2.
PD 03-JAN-2002.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 3.9%; Score 34.6; DB 6; Length 18826;
Best Local Similarity 54.3%; Pred. No. 56;
RESULT 278
ID AAD42260 standard; cDNA; 613 BP.
DE Corn FT homologue cDNA from clone cta1n.pk0058.d11b.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.9%; Score 34.4; DB 6; Length 613;
Best Local Similarity 58.7%; Pred. No. 10;
RESULT 279
ID ADR04286 standard; cDNA; 613 BP.
DE Corn FT homologue encoding cDNA SEQ ID NO:53.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.9%; Score 34.4; DB 13; Length 613;
Best Local Similarity 58.7%; Pred. No. 10;
RESULT 280
ID ADC03435 standard; DNA; 413 BP.
DE Banana flowering time-related DNA sequence #9.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.8%; Score 34.2; DB 10; Length 413;
Best Local Similarity 64.6%; Pred. No. 9.5;
RESULT 281
ID ABX48443 standard; cDNA; 426 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13608.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.8%; Score 34.2; DB 8; Length 426;
Best Local Similarity 52.4%; Pred. No. 9.7;
RESULT 282
ID ADC03497 standard; DNA; 555 BP.
DE Rice flowering time-related gene #41.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.8%; Score 34.2; DB 10; Length 555;
Best Local Similarity 62.1%; Pred. No. 11;
RESULT 283
ID AAD42252 standard; cDNA; 850 BP.
DE Soybean FT homologue cDNA #1.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.8%; Score 34.2; DB 6; Length 850;
Best Local Similarity 60.0%; Pred. No. 14;
RESULT 284
ID ADR04268 standard; cDNA; 850 BP.
DE Soybean FT homologue encoding cDNA SEQ ID NO:35.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.8%; Score 34.2; DB 13; Length 850;
Best Local Similarity 60.0%; Pred. No. 14;
RESULT 285
ID ADT45696 standard; cDNA; 3735 BP.
DE Bacterial polynucleotide #20447.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.8%; Score 34.2; DB 13; Length 3735;
Best Local Similarity 46.4%; Pred. No. 31;
RESULT 286
ID ADP74211 standard; DNA; 149158 BP.
DE Equine herpesvirus 1 genome gM deletion mutant #2.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.8%; Score 34.2; DB 12; Length 149158;
Best Local Similarity 47.4%; Pred. No. 2.2e+02;
RESULT 287
ID ADP74212 standard; DNA; 149261 BP.
DE Equine herpesvirus 1 genome gM deletion mutant #3.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.8%; Score 34.2; DB 12; Length 149261;
Best Local Similarity 47.4%; Pred. No. 2.2e+02;
RESULT 288
ID ADP74216 standard; DNA; 150071 BP.
DE Equine herpesvirus 1 genome gM deletion mutant #1.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.8%; Score 34.2; DB 12; Length 150071;
Best Local Similarity 47.4%; Pred. No. 2.3e+02;
RESULT 289
ID ADP74201 standard; DNA; 150223 BP.
DE Equine herpesvirus 1 genome seqid 1.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.8%; Score 34.2; DB 12; Length 150223;
Best Local Similarity 47.4%; Pred. No. 2.3e+02;
RESULT 290
ID AAS45458 standard; DNA; 13606 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #82.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 34; DB 4; Length 13606;
Best Local Similarity 61.1%; Pred. No. 72;
RESULT 291
ID AAS46562 standard; DNA; 13606 BP.
DE Tumour suppressor gene derived chemically modified sequence #284.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 34; DB 4; Length 13606;
Best Local Similarity 61.1%; Pred. No. 72;
RESULT 292
ID ABL33811 standard; DNA; 13606 BP.
DE Human immune system associated gene SEQ ID NO: 1784.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 34; DB 6; Length 13606;
Best Local Similarity 61.1%; Pred. No. 72;
RESULT 293
ID ABK28314 standard; DNA; 13606 BP.
DE DNA transcription associated complementary genomic DNA #94.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 34; DB 6; Length 13606;
Best Local Similarity 61.1%; Pred. No. 72;
RESULT 294
ID ADQ30844 standard; cDNA; 730 BP.
DE Pea floral development gene PsTFL1a coding sequence.
PN EP1439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 3.8%; Score 33.8; DB 12; Length 730;
Best Local Similarity 52.5%; Pred. No. 17;
RESULT 295
ID ABL27595 standard; DNA; 1083 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 34258.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 33.8; DB 4; Length 1083;
Best Local Similarity 62.4%; Pred. No. 21;
RESULT 296
ID ABL27594 standard; DNA; 3144 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 34255.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 33.8; DB 4; Length 3144;
Best Local Similarity 62.4%; Pred. No. 38;
RESULT 297
ID ABL27592 standard; DNA; 5436 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 34249.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 33.8; DB 4; Length 5436;
Best Local Similarity 62.4%; Pred. No. 51;
RESULT 298
ID ABX36799 standard; cDNA; 426 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1964.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.8%; Score 33.6; DB 8; Length 426;
Best Local Similarity 52.1%; Pred. No. 15;
RESULT 299
ID ADB57541 standard; DNA; 667 BP.
DE Toxicity-related gene, SEQ ID 2567.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 33.6; DB 10; Length 667;
Best Local Similarity 50.6%; Pred. No. 19;
RESULT 300
ID ADB52060 standard; DNA; 667 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2602.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 33.6; DB 10; Length 667;
Best Local Similarity 50.6%; Pred. No. 19;
RESULT 301
ID ADP72364 standard; DNA; 667 BP.
DE Renal toxin progression gene marker #953.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 33.6; DB 12; Length 667;
Best Local Similarity 50.6%; Pred. No. 19;

RESULT 302
ID ABX14651 standard; cDNA; 1606 BP.
DE Human cDNA encoding squalene synthase.
PN US2002142418-A1.
PD 03-OCT-2002.
PA (WEIM/) WEI M.
PA (YANC/) YAN C.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 3.8%; Score 33.6; DB 8; Length 1606;
Best Local Similarity 51.3%; Pred. No. 30;
RESULT 303
ID ADN96861 standard; cDNA; 1606 BP.
DE Novel human enzyme cDNA.
PN US2004106179-A1.
PD 03-JUN-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.8%; Score 33.6; DB 12; Length 1606;
Best Local Similarity 51.3%; Pred. No. 30;
RESULT 304
ID ADB53939 standard; DNA; 1644 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4481.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 33.6; DB 10; Length 1644;
Best Local Similarity 50.6%; Pred. No. 31;
RESULT 305
ID ABT42500 standard; DNA; 1644 BP.
DE Toxicity modelling related rat gene SEQ ID No 2202.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 33.6; DB 10; Length 1644;
Best Local Similarity 50.6%; Pred. No. 31;
RESULT 306
ID ADP73017 standard; DNA; 1644 BP.
DE Renal toxin progression gene marker #1606.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 33.6; DB 12; Length 1644;
Best Local Similarity 50.6%; Pred. No. 31;
RESULT 307
ID AAS94917 standard; DNA; 2097 BP.
DE Human DNA sequence #172 expressed during foam cell differentiation.
PN WO200177389-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.8%; Score 33.6; DB 6; Length 2097;
Best Local Similarity 51.3%; Pred. No. 35;
RESULT 308
ID ADI61662 standard; cDNA; 2097 BP.
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 350423.5.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.8%; Score 33.6; DB 12; Length 2097;
Best Local Similarity 51.3%; Pred. No. 35;
RESULT 309
ID ADM03547 standard; cDNA; 2884 BP.
DE Human cDNA of the invention SEQ ID NO:2232.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.8%; Score 33.6; DB 11; Length 2884;
Best Local Similarity 56.2%; Pred. No. 42;
RESULT 310
ID ACL23170 standard; DNA; 406 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13161.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 406;
Best Local Similarity 57.0%; Pred. No. 17;
RESULT 311
ID ACL23160 standard; DNA; 514 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13151.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 514;
Best Local Similarity 57.0%; Pred. No. 19;
RESULT 312
ID ACL23162 standard; DNA; 516 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13153.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 516;
Best Local Similarity 57.0%; Pred. No. 19;
RESULT 313
ID ACL23156 standard; DNA; 538 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13147.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 538;
Best Local Similarity 57.0%; Pred. No. 20;
RESULT 314
ID ACL23164 standard; DNA; 548 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13155.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 548;
Best Local Similarity 57.0%; Pred. No. 20;
RESULT 315
ID ACL23143 standard; DNA; 590 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13134.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 590;
Best Local Similarity 57.0%; Pred. No. 21;
RESULT 316
ID ACL23167 standard; DNA; 608 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13158.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 608;
Best Local Similarity 57.0%; Pred. No. 21;
RESULT 317
ID ACL23169 standard; DNA; 617 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13160.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 617;
Best Local Similarity 57.0%; Pred. No. 21;
RESULT 318
ID ACL23148 standard; DNA; 623 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13139.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 623;
Best Local Similarity 57.0%; Pred. No. 21;
RESULT 319
ID ACL23157 standard; DNA; 631 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13148.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.8%; Score 33.4; DB 9; Length 631;

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  Best Local Similarity   57.0%;  Pred. No. 21;
RESULT 320
ID   ACL23168 standard; DNA; 637 BP.
DE   DNA clone originating in barley containing SNP encoding sequence #13159.
PN   WO2003057877-A1.
PD   17-JUL-2003.
PA   (UYNI-) UNIV JAPAN OKAYAMA.
  Query Match             3.8%;  Score 33.4;  DB 9;  Length 637;
  Best Local Similarity   57.0%;  Pred. No. 21;
RESULT 321
ID   ACL23158 standard; DNA; 655 BP.
DE   DNA clone originating in barley containing SNP encoding sequence #13149.
PN   WO2003057877-A1.
PD   17-JUL-2003.
PA   (UYNI-) UNIV JAPAN OKAYAMA.
  Query Match             3.8%;  Score 33.4;  DB 9;  Length 655;
  Best Local Similarity   57.0%;  Pred. No. 22;
RESULT 322
ID   ADH13064 standard; DNA; 678 BP.
DE   E coli ribulose-phosphate 3 epimerase gene SeqID15.
PN   WO2003084986-A2.
PD   16-OCT-2003.
PA   (AFFI-) AFFINIUM PHARM INC.
  Query Match             3.8%;  Score 33.4;  DB 10;  Length 678;
  Best Local Similarity   57.0%;  Pred. No. 22;
RESULT 323
ID   ADH13062 standard; DNA; 678 BP.
DE   E coli ribulose-phosphate 3 epimerase gene SeqID13.
PN   WO2003084986-A2.
PD   16-OCT-2003.
PA   (AFFI-) AFFINIUM PHARM INC.
  Query Match             3.8%;  Score 33.4;  DB 10;  Length 678;
  Best Local Similarity   57.0%;  Pred. No. 22;
RESULT 324
ID   ACL23163 standard; DNA; 679 BP.
DE   DNA clone originating in barley containing SNP encoding sequence #13154.
PN   WO2003057877-A1.
PD   17-JUL-2003.
PA   (UYNI-) UNIV JAPAN OKAYAMA.
  Query Match             3.8%;  Score 33.4;  DB 9;  Length 679;
  Best Local Similarity   57.0%;  Pred. No. 22;
RESULT 325
ID   ACL23145 standard; DNA; 681 BP.
DE   DNA clone originating in barley containing SNP encoding sequence #13136.
PN   WO2003057877-A1.
PD   17-JUL-2003.
PA   (UYNI-) UNIV JAPAN OKAYAMA.
  Query Match             3.8%;  Score 33.4;  DB 9;  Length 681;
  Best Local Similarity   57.0%;  Pred. No. 22;
RESULT 326
ID   ACL23161 standard; DNA; 692 BP.
DE   DNA clone originating in barley containing SNP encoding sequence #13152.
PN   WO2003057877-A1.
PD   17-JUL-2003.
PA   (UYNI-) UNIV JAPAN OKAYAMA.
  Query Match             3.8%;  Score 33.4;  DB 9;  Length 692;
  Best Local Similarity   57.0%;  Pred. No. 22;
RESULT 327
ID   ACL23159 standard; DNA; 717 BP.
DE   DNA clone originating in barley containing SNP encoding sequence #13150.
PN   WO2003057877-A1.
PD   17-JUL-2003.
PA   (UYNI-) UNIV JAPAN OKAYAMA.
  Query Match             3.8%;  Score 33.4;  DB 9;  Length 717;
  Best Local Similarity   57.0%;  Pred. No. 23;
RESULT 328
ID   AAQ23646 standard; DNA; 1032 BP.
DE   Acetylpolyamine amidohydrolase gene.
PN   JP04071489-A.
PD   06-MAR-1992.
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
  Query Match             3.8%;  Score 33.4;  DB 2;  Length 1032;
  Best Local Similarity   48.7%;  Pred. No. 28;
RESULT 329
ID   AAS90148 standard; cDNA; 3639 BP.
DE   DNA encoding novel human diagnostic protein #25952.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.8%;  Score 33.4;  DB 5;  Length 3639;
  Best Local Similarity   57.0%;  Pred. No. 54;
RESULT 330
ID   AAS68242 standard; cDNA; 3639 BP.
DE   DNA encoding novel human diagnostic protein #4046.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.8%;  Score 33.4;  DB 5;  Length 3639;
  Best Local Similarity   57.0%;  Pred. No. 54;
RESULT 331
  Query Match             3.8%;  Score 33.4;  DB 12;  Length 110000;
  Best Local Similarity   53.8%;  Pred. No. 3.4e+02;
RESULT 332
ID   ACH19525 standard; cDNA; 405 BP.
DE   Human adult lung cDNA #528.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.7%;  Score 33.2;  DB 9;  Length 405;
  Best Local Similarity   46.8%;  Pred. No. 19;
RESULT 333
ID   ACH19428 standard; cDNA; 409 BP.
DE   Human adult lung cDNA #431.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.7%;  Score 33.2;  DB 9;  Length 409;
  Best Local Similarity   46.8%;  Pred. No. 19;
RESULT 334
ID   ACH19701 standard; cDNA; 411 BP.
DE   Human adult lung cDNA #704.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.7%;  Score 33.2;  DB 9;  Length 411;
  Best Local Similarity   46.8%;  Pred. No. 20;
RESULT 335
ID   ADD45916 standard; DNA; 413 BP.
DE   Rat gene AI009191, SEQ ID NO 11586.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             3.7%;  Score 33.2;  DB 10;  Length 413;
  Best Local Similarity   55.1%;  Pred. No. 20;
RESULT 336
ID   ACH19800 standard; cDNA; 420 BP.
DE   Human adult lung cDNA #803.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
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PA (JONE/) JONES L W.
Query Match 3.7%; Score 33.2; DB 9; Length 420;
Best Local Similarity 46.8%; Pred. No. 20;
RESULT 337
ID ADM47218 standard; DNA; 590 BP.
DE Surfactant protein-C like NOVX 12b gene.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.7%; Score 33.2; DB 11; Length 590;
Best Local Similarity 46.8%; Pred. No. 24;
RESULT 338
ID ABX94301 standard; cDNA; 616 BP.
DE Human cDNA encoding surfactant protein C, SP-C.
PN US2002197646-A1.
PD 26-DEC-2002.
PA (NOGE/) NOGEE L M.
PA (COLE/) COLE F S.
PA (WHIT/) WHITSETT J A.
PA (HAMV/) HAMVAS A.
Query Match 3.7%; Score 33.2; DB 9; Length 616;
Best Local Similarity 46.8%; Pred. No. 24;
RESULT 339
ID AAN70715 standard; DNA; 852 BP.
DE Sequence encoding a canine 5 kd alveolar surfactant protein (ASP) from
DE clone cDNA #19.
PN WO8706588-A.
PD 05-NOV-1987.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 1; Length 852;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 340
ID AAN80721 standard; DNA; 852 BP.
DE Human SP5 #19.
PN WO8805820-A.
PD 11-AUG-1988.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 1; Length 852;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 341
ID AAN90094 standard; cDNA; 852 BP.
DE ss cDNA number 19 encoding human SP-5-derived protein.
PN WO8904326-A.
PD 18-MAY-1989.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 1; Length 852;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 342
ID AAQ15263 standard; cDNA; 852 BP.
DE SP-5 clone #19.
PN WO9118015-A.
PD 28-NOV-1991.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 2; Length 852;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 343
ID AAI94259 standard; cDNA; 854 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 334.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 3.7%; Score 33.2; DB 4; Length 854;
Best Local Similarity 54.6%; Pred. No. 29;
RESULT 344
ID ABT32161 standard; DNA; 854 BP.
DE Human neuroblastoma-related DNA sequence #7.
PN WO200297093-A1.
PD 05-DEC-2002.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 3.7%; Score 33.2; DB 8; Length 854;
Best Local Similarity 54.6%; Pred. No. 29;
RESULT 345
ID AAN80641 standard; cDNA; 858 BP.
DE Sequence of a complete pulmonary hydrophobic surfactant-associated
DE protein (SAP) (Val) human cDNA.
PN WO8803170-A.
PD 05-MAY-1988.
PA (WHIT/) WHITSETT J A.
PA (ABBO) ABBOTT LAB.
Query Match 3.7%; Score 33.2; DB 1; Length 858;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 346
ID AAN90099 standard; cDNA; 858 BP.
DE ss cDNA number 18 encoding human SP-5-derived protein.
PN WO8904326-A.
PD 18-MAY-1989.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 1; Length 858;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 347
ID AAN70714 standard; DNA; 861 BP.
DE Sequence encoding a canine 5 kd alveolar surfactant protein (ASP) from
DE clone cDNA #18.
PN WO8706588-A.
PD 05-NOV-1987.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 1; Length 861;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 348
ID AAN80720 standard; cDNA; 861 BP.
DE Human SP5 #18.
PN WO8805820-A.
PD 11-AUG-1988.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 1; Length 861;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 349
ID AAQ15262 standard; cDNA; 861 BP.
DE SP-5 clone #18.
PN WO9118015-A.
PD 28-NOV-1991.
PA (CALD) CALIFORNIA BIOTECHNOLOGY INC.
Query Match 3.7%; Score 33.2; DB 2; Length 861;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 350
ID ADG32821 standard; DNA; 876 BP.
DE Human DNA differentially expressed in patients with SLE SeqID145.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 3.7%; Score 33.2; DB 10; Length 876;
Best Local Similarity 46.8%; Pred. No. 29;
RESULT 351
ID AAD42240 standard; cDNA; 899 BP.
DE Corn FT homologue cDNA from clone cco1n.pk0037.d10.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.7%; Score 33.2; DB 6; Length 899;
Best Local Similarity 61.6%; Pred. No. 30;
RESULT 352
ID ADR04244 standard; cDNA; 899 BP.
DE Corn FT homologue encoding cDNA SEQ ID NO:11.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.7%; Score 33.2; DB 13; Length 899;
Best Local Similarity 61.6%; Pred. No. 30;
RESULT 353
ID AAF18020 standard; DNA; 926 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 39.
PN WO200055180-A2.
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 3.7%; Score 33.2; DB 3; Length 926;
Best Local Similarity 46.8%; Pred. No. 30;
RESULT 354
ID ADK70288 standard; cDNA; 1321 BP.
DE Respiratory disease differentially expressed cDNA #24.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 33.2; DB 12; Length 1321;
Best Local Similarity 46.8%; Pred. No. 37;
RESULT 355
ID ADG10839 standard; cDNA; 1641 BP.
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:429.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 3.7%; Score 33.2; DB 10; Length 1641;
Best Local Similarity 52.1%; Pred. No. 41;
RESULT 356
ID ABX34790 standard; cDNA; 1652 BP.
DE Human mddt cDNA SEQ ID 351.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 33.2; DB 8; Length 1652;
Best Local Similarity 46.8%; Pred. No. 41;
RESULT 357
ID ADG10727 standard; cDNA; 1762 BP.
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:317.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 3.7%; Score 33.2; DB 10; Length 1762;
Best Local Similarity 52.1%; Pred. No. 43;
RESULT 358
ID AAS62260 standard; cDNA; 2588 BP.
DE cDNA sequence #47 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 3.7%; Score 33.2; DB 6; Length 2588;
Best Local Similarity 52.1%; Pred. No. 52;
RESULT 359
ID ADC03483 standard; DNA; 522 BP.
DE Rice flowering time-related gene #34.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 33; DB 10; Length 522;
Best Local Similarity 52.6%; Pred. No. 26;
RESULT 360
ID ADS62020 standard; cDNA; 627 BP.
DE Bacterial polynucleotide #14007.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.7%; Score 33; DB 13; Length 627;
Best Local Similarity 58.8%; Pred. No. 28;
RESULT 361
ID AAT30564 standard; cDNA; 1585 BP.
DE Eukaryotic cell growth inhibiting factor cDNA clone pTB1848.
PN WO9617933-A2.
PD 13-JUN-1996.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 3.7%; Score 33; DB 2; Length 1585;
Best Local Similarity 55.8%; Pred. No. 46;
RESULT 362
ID ABI99326 standard; cDNA; 2902 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:195.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 3.7%; Score 33; DB 6; Length 2902;
Best Local Similarity 51.0%; Pred. No. 64;
RESULT 363
ID ADJ75755 standard; DNA; 2902 BP.
DE Marker gene SEQ ID NO:1007.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 3.7%; Score 33; DB 12; Length 2902;
Best Local Similarity 51.0%; Pred. No. 64;
RESULT 364
ID ADQ64615 standard; cDNA; 4118 BP.
DE Novel human cDNA sequence #1776.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.7%; Score 33; DB 12; Length 4118;
Best Local Similarity 50.3%; Pred. No. 78;
RESULT 365
ID ABV96068 standard; cDNA; 226 BP.
DE Human pancreatic cancer expressed cDNA SEQ ID NO 1476.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.7%; Score 32.8; DB 6; Length 226;
Best Local Similarity 51.0%; Pred. No. 19;
RESULT 366
ID ABX88312 standard; cDNA; 282 BP.
DE Corn ear-derived polynucleotide (cpd) #6772.
PN US6476212-B1.
PD 05-NOV-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 32.8; DB 10; Length 282;
Best Local Similarity 50.6%; Pred. No. 21;
RESULT 367
ID AAT25911 standard; cDNA to mRNA; 359 BP.
DE Human gene signature HUMGS08142.
PN WO9514772-A1.
PD 01-JUN-1995.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
Query Match 3.7%; Score 32.8; DB 2; Length 359;
Best Local Similarity 50.7%; Pred. No. 24;
RESULT 368
ID AAL02502 standard; cDNA; 441 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2503.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 32.8; DB 4; Length 441;
Best Local Similarity 53.2%; Pred. No. 27;
RESULT 369
ID ABL97268 standard; cDNA; 441 BP.
DE Human testicular antigen encoding cDNA SEQ ID NO: 936.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 32.8; DB 4; Length 441;
Best Local Similarity 53.2%; Pred. No. 27;
RESULT 370
ID ADL67133 standard; cDNA; 781 BP.
DE Human B7-H4LV(ECD) encoding cDNA SEQ ID NO:3.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 3.7%; Score 32.8; DB 12; Length 781;
Best Local Similarity 51.4%; Pred. No. 37;
RESULT 371

ID AAQ14832 standard; cDNA; 822 BP.
DE OV-16 antigen.
PN USN7644372-N.
PD 05-NOV-1991.
PA (USSH) NAT INST OF HEALTH.
Query Match 3.7%; Score 32.8; DB 2; Length 822;
Best Local Similarity 53.0%; Pred. No. 38;
RESULT 372
ID ADL67131 standard; cDNA; 970 BP.
DE Human B7-H4LV encoding cDNA SEQ ID NO:1.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 3.7%; Score 32.8; DB 12; Length 970;
Best Local Similarity 51.4%; Pred. No. 41;
RESULT 373
ID ABZ59671 standard; cDNA; 1278 BP.
DE Human secreted protein SECP-26 encoding cDNA SEQ ID NO:57.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYY/) LU Y.
Query Match 3.7%; Score 32.8; DB 9; Length 1278;
Best Local Similarity 51.4%; Pred. No. 48;
RESULT 374
ID ABK94918 standard; cDNA; 1413 BP.
DE Human novel polynucleotide #29.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 3.7%; Score 32.8; DB 6; Length 1413;
Best Local Similarity 51.4%; Pred. No. 50;
RESULT 375
ID ADA53734 standard; cDNA; 2199 BP.
DE Human coding sequence, SEQ ID 1302.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.7%; Score 32.8; DB 10; Length 2199;
Best Local Similarity 51.4%; Pred. No. 64;
RESULT 376
ID ACN92904 standard; DNA; 2429 BP.
DE Breast cancer related marker, seq id 14054.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.7%; Score 32.8; DB 11; Length 2429;
Best Local Similarity 54.0%; Pred. No. 67;
RESULT 377
ID AAS21305 standard; cDNA; 3479 BP.
DE Human cDNA sequence encoding for PRO4346 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 4; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 378
ID ACA03664 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 8; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 379
ID ABX89202 standard; cDNA; 3479 BP.
DE DNA encoding novel secreted and transmembrane protein PRO4346.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 8; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 380
ID ACD41856 standard; cDNA; 3479 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #62.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 8; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 381
ID ACA04085 standard; cDNA; 3479 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 123.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 8; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 382
ID ADA45642 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 383
ID ADA76073 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 384
ID ADA18723 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 385
ID ADA61346 standard; cDNA; 3479 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 386
ID ADB19131 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 387
ID ADB27672 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 388
ID ADA86151 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 389

ID ADB15715 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 390
ID ADA47501 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 391
ID ADA67296 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 392
ID ADB30303 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 393
ID ADA85599 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 394
ID ADA96811 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 395
ID ADA79115 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 396
ID ADA87254 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 397
ID ADB16456 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 398
ID ADA91548 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 399
ID ADB14611 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 400
ID ADB18572 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 401
ID ADA93787 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 402
ID ADB19683 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 403
ID ADB12995 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 404
ID ACD98485 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 405
ID ADA74249 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 406
ID ADB24482 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 407
ID ADA82006 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.

PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 408
ID ADA74969 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 409
ID ADA85047 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 410
ID ADA84495 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 411
ID ADB29751 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 412
ID ADA80279 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 413
ID ADA75521 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 414
ID ADA46746 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 415
ID ADB25042 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 416
ID ADA93218 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 417
ID ADB26568 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 418
ID ADB30855 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 419
ID ADA60783 standard; cDNA; 3479 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 420
ID ADB23930 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 421
ID ADA96259 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 422
ID ADA80831 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 423
ID ADA95707 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 424
ID ADB26016 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 425
ID ADB21501 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 426
ID ADA77280 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 427
ID ADB18020 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 428
ID ADA86703 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 429
ID ADA87806 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 430
ID ADA46194 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 431
ID ADB28224 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 432
ID ADB28776 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 433
ID ADA76728 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 434
ID ADA88358 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 435
ID ADA97363 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 436
ID ADB27120 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 437
ID ADB22053 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 438
ID ADA66744 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 439
ID ADB22605 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 440
ID ADB23378 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 441
ID ADA92100 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 442
ID ADB15163 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 443
ID ADB38415 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 444

ID ADB37863 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 9; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 445
ID ADB66335 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 446
ID ADB89415 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 447
ID ADB90147 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 448
ID ADB39248 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 449
ID ADB46871 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 450
ID ADB86478 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 451
ID ADB77083 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 452
ID ADB34240 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 453
ID ADB35344 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 454
ID ADB33688 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 455
ID ADB34792 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 456
ID ADB35896 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide SEQ ID NO 123.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 457
ID ADB46291 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 458
ID ADC50164 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 459
ID ADC71711 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 460
ID ADC59690 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 461
ID ADC52697 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID123.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 462
ID ADC57051 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID123.

PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 463
ID ADC60242 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 464
ID ADC50717 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 465
ID ADC65244 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 466
ID ADC54342 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID123.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 467
ID ADC53303 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID123.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 468
ID ADC58826 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID123.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 469
ID ADC55704 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID123.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 470
ID ADC58274 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID123.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 471
ID ADD02948 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 472
ID ADC89940 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 473
ID ADC69359 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 474
ID ADC48248 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 475
ID ADD09777 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 476
ID ADD04352 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 477
ID ADC80308 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 478
ID ADD10815 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 479
ID ADC47696 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 480
ID ADC79756 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 481
ID ADD09225 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 482
ID ADD40938 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 483
ID ADD52077 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 484
ID ADD52817 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 485
ID ADD53369 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 486
ID ADD51525 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 487
ID ADD02324 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 488
ID ADD01758 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 489
ID ADD53940 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 490
ID ADD92257 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 491
ID ADD91153 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 492
ID ADE03767 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 493
ID ADE32064 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 494
ID ADE21996 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 495
ID ADD79220 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 496
ID ADE41756 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 497
ID ADE17573 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 498
ID ADD91705 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;

Best Local Similarity 51.4%; Pred. No. 82;
RESULT 499
ID ADE33168 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 500
ID ADE33720 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 501
ID ADD79772 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 502
ID ADD92809 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 503
ID ADE19229 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 504
ID ADE18677 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 505
ID ADE42873 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 506
ID ADD95662 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 507
ID ADE22548 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 508
ID ADD78666 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 509
ID ADE32616 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 510
ID ADE42308 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 511
ID ADD80324 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 512
ID ADD89352 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 513
ID ADE40636 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 514
ID ADE04435 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 515
ID ADE92564 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 516
ID ADG21273 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 517

ID ADG22914 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 518
ID ADF97249 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 519
ID ADG80313 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 520
ID ADG79761 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 521
ID ADH55053 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 522
ID ADH55605 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 523
ID ADI64773 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 524
ID ADI63272 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 525
ID ADH81686 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 526
ID ADH81134 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 527
ID ACD23914 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 528
ID ACA67055 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 10; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 529
ID ADM82303 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 11; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 530
ID ADN15702 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 11; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 531
ID ADN16331 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 11; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 532
ID ADN15150 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 11; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 533
ID ADN14598 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 11; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 534
ID ADI63824 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 11; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 535
ID ADC80860 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.

PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 536
ID ADD76308 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 537
ID ADD87672 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 538
ID ADD86076 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 539
ID ADE75524 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 540
ID ADE23100 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 541
ID ADE23652 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 542
ID ADE24295 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 543
ID ADD87120 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 544
ID ADE88986 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 545
ID ADE18125 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 546
ID ADE88434 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 547
ID ADE94454 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 548
ID ADE90865 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 549
ID ADE95006 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 550
ID ADE93116 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 551
ID ADF34697 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 552
ID ADE92012 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 553
ID ADE90313 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003199063-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 554
ID ADE91460 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 555
ID ADG02039 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 556
ID ADG21825 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 557
ID ADG19895 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 558
ID ADF97801 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 559
ID ADG24018 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 560
ID ADF98372 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 561
ID ADG03203 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 562
ID ADF98924 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 563
ID ADG16509 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 564
ID ADG04968 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 565
ID ADG19235 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 566
ID ADG13072 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 567
ID ADG08129 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 568
ID ADG15299 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 569
ID ADF96697 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 570
ID ADG05882 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 571
ID ADG23466 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;

Best Local Similarity 51.4%; Pred. No. 82;
RESULT 572
ID ADG03755 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 573
ID ADG24656 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 574
ID ADG06953 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 575
ID ADG07505 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 576
ID ADG55000 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 577
ID ADG60664 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 578
ID ADG61768 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 579
ID ADG81969 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 580
ID ADG57208 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 581
ID ADG56656 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 582
ID ADG55552 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 583
ID ADG58312 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 584
ID ADG70678 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 585
ID ADG57760 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 586
ID ADG53344 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 587
ID ADG71230 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 588
ID ADG81417 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 589
ID ADH30379 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 590
ID ADH11746 standard; cDNA; 3479 BP.

DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 591
ID ADG52168 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 592
ID ADG53896 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 593
ID ADG80865 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 594
ID ADG56104 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 595
ID ADH12370 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 596
ID ADG61216 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 597
ID ADH28303 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 598
ID ADG54448 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 599
ID ADG59488 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 600
ID ADI80912 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 601
ID ADG09655 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 602
ID ADI15126 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 603
ID ADG09003 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 604
ID ADI14458 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 605
ID ADI18053 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 606
ID ADJ63334 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 607
ID ADJ77229 standard; cDNA; 3479 BP.
DE Human PRO polynucleotide #62.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 608
ID ADJ65351 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2004038335-A1.

PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 609
ID ADM27487 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 610
ID ADM42211 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 611
ID ADM28073 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 12; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 612
ID ADI95555 standard; cDNA; 3479 BP.
DE cDNA encoding human PRO polypeptide #62.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 13; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 613
ID ADI96107 standard; cDNA; 3479 BP.
DE Novel human secreted and transmembrane protein PRO4346 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 32.8; DB 13; Length 3479;
Best Local Similarity 51.4%; Pred. No. 82;
RESULT 614
ID AAK98324 standard; DNA; 9905 BP.
DE Human purinergic-related G-protein coupled receptor (GPCR) genomic DNA.
PN WO200187980-A2.
PD 22-NOV-2001.
PA (APPL-) APPLERA CORP.
Query Match 3.7%; Score 32.8; DB 6; Length 9905;
Best Local Similarity 46.5%; Pred. No. 1.4e+02;
RESULT 615
ID ADL67148 standard; DNA; 10561 BP.
DE Plasmid pCEP-hsB7-H4(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:18.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 3.7%; Score 32.8; DB 12; Length 10561;
Best Local Similarity 51.4%; Pred. No. 1.5e+02;
RESULT 616
ID ADL67147 standard; DNA; 11006 BP.
DE Plasmid pCEP-hsB7-H4(ECD)-Fc nucleotide sequence SEQ ID NO:17.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 3.7%; Score 32.8; DB 12; Length 11006;
Best Local Similarity 51.4%; Pred. No. 1.5e+02;
RESULT 617
ID ADK55918 standard; DNA; 298 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3301.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.7%; Score 32.6; DB 10; Length 298;
Best Local Similarity 55.9%; Pred. No. 25;
RESULT 618
ID ABV60840 standard; cDNA; 406 BP.
DE Human prostate expression marker cDNA 60831.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.7%; Score 32.6; DB 5; Length 406;
Best Local Similarity 80.9%; Pred. No. 30;
RESULT 619
ID ADF50992 standard; cDNA; 871 BP.
DE Human HN1 cDNA clone (SeqID 91).
PN WO2003060164-A1.
PD 24-JUL-2003.
PA (ARCT-) ARCTURUS ENG INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.7%; Score 32.6; DB 10; Length 871;
Best Local Similarity 50.3%; Pred. No. 45;
RESULT 620
ID ACA27201 standard; DNA; 1260 BP.
DE Prokaryotic essential gene #8858.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.7%; Score 32.6; DB 8; Length 1260;
Best Local Similarity 58.9%; Pred. No. 55;
RESULT 621
ID ADR07008 standard; cDNA; 4233 BP.
DE Full length human cDNA useful for treating neurological disease Seq 514.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.7%; Score 32.6; DB 13; Length 4233;
Best Local Similarity 52.6%; Pred. No. 1e+02;
RESULT 622
ID ABA18621 standard; DNA; 8227 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10952.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 32.6; DB 5; Length 8227;
Best Local Similarity 51.7%; Pred. No. 1.5e+02;
RESULT 623
ID ABL20639 standard; DNA; 598 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 32.4; DB 4; Length 598;
Best Local Similarity 51.4%; Pred. No. 42;
RESULT 624
ID ADQ97241 standard; DNA; 1159 BP.
DE Mouse cancer associated sequence MR08-019, SEQ ID 217.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 32.4; DB 12; Length 1159;
Best Local Similarity 53.1%; Pred. No. 60;
RESULT 625
ID AAS78904 standard; cDNA; 1668 BP.
DE DNA encoding novel human diagnostic protein #14708.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 32.4; DB 5; Length 1668;
Best Local Similarity 50.6%; Pred. No. 74;
RESULT 626
ID ABA03490 standard; DNA; 1747 BP.
DE Human N-acetyl-glucosaminyl transferase III regulatory sequence.
PN KR97021309-A.

PD 28-MAY-1997.
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
Query Match 3.6%; Score 32.4; DB 2; Length 1747;
Best Local Similarity 56.6%; Pred. No. 75;
RESULT 627
ID ABL20638 standard; DNA; 2598 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13387.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 32.4; DB 4; Length 2598;
Best Local Similarity 51.4%; Pred. No. 93;
RESULT 628
ID ABL12202 standard; cDNA; 2827 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31088.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 32.4; DB 4; Length 2827;
Best Local Similarity 51.4%; Pred. No. 98;
RESULT 629
ID ABL09312 standard; cDNA; 2837 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22418.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 32.4; DB 4; Length 2837;
Best Local Similarity 51.4%; Pred. No. 98;
RESULT 630
ID ADN94933 standard; DNA; 2889 BP.
DE Indian rice Kasalath variety flowering-related RFT1 gDNA.
PN JP2004089036-A.
PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 3.6%; Score 32.4; DB 12; Length 2889;
Best Local Similarity 50.0%; Pred. No. 99;
RESULT 631
ID ADN94936 standard; DNA; 2907 BP.
DE Japanese rice Nipponbare variety flowering-related RFT1 gDNA.
PN JP2004089036-A.
PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 3.6%; Score 32.4; DB 12; Length 2907;
Best Local Similarity 50.0%; Pred. No. 99;
RESULT 632
ID ADS89739 standard; DNA; 3036 BP.
DE Oligonucleotide of the invention SEQ ID NO:755.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 32.4; DB 13; Length 3036;
Best Local Similarity 48.9%; Pred. No. 1e+02;
RESULT 633
ID AAK74236 standard; DNA; 3061 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29048.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 32.4; DB 4; Length 3061;
Best Local Similarity 50.0%; Pred. No. 1e+02;
RESULT 634
ID ADE61938 standard; DNA; 3225 BP.
DE Human gene NM_032294, SEQ ID NO 7867.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 32.4; DB 10; Length 3225;
Best Local Similarity 56.6%; Pred. No. 1e+02;
RESULT 635
ID ADE61942 standard; DNA; 3225 BP.
DE Human gene NM_032294, SEQ ID NO 7871.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 32.4; DB 10; Length 3225;
Best Local Similarity 56.6%; Pred. No. 1e+02;
RESULT 636
ID ADE56971 standard; DNA; 3299 BP.
DE Rat gene L07925, SEQ ID NO 2826.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 32.4; DB 10; Length 3299;
Best Local Similarity 50.6%; Pred. No. 1.1e+02;
RESULT 637
ID ADE56967 standard; DNA; 3299 BP.
DE Rat gene L07925, SEQ ID NO 2822.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 32.4; DB 10; Length 3299;
Best Local Similarity 50.6%; Pred. No. 1.1e+02;
RESULT 638
ID ADD45417 standard; DNA; 3299 BP.
DE Rat gene L07925, SEQ ID NO 10850.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 32.4; DB 10; Length 3299;
Best Local Similarity 50.6%; Pred. No. 1.1e+02;
RESULT 639
ID ADQ97240 standard; DNA; 28449 BP.
DE Mouse cancer associated sequence MD08-019, SEQ ID 216.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 32.4; DB 12; Length 28449;
Best Local Similarity 53.1%; Pred. No. 3.4e+02;
RESULT 640
ID ABK83568 standard; DNA; 201143 BP.
DE Human DNA differentially expressed in granulocytic cells #139.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 32.4; DB 6; Length 201143;
Best Local Similarity 54.1%; Pred. No. 9.5e+02;
RESULT 641
ID ABX47026 standard; cDNA; 380 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12191.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.6%; Score 32.2; DB 8; Length 380;
Best Local Similarity 52.6%; Pred. No. 38;
RESULT 642
ID ADR01806 standard; DNA; 863 BP.
DE A. gossypii genomic DNA PAG1351UP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 32.2; DB 2; Length 863;
Best Local Similarity 56.5%; Pred. No. 60;
RESULT 643
ID ADJ44103 standard; cDNA; 980 BP.

DE Plant cDNA #5103.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 3.6%; Score 32.2; DB 12; Length 980;
Best Local Similarity 52.6%; Pred. No. 64;
RESULT 644
ID ADN63226 standard; DNA; 1098 BP.
DE Human NOV55c DNA.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 3.6%; Score 32.2; DB 12; Length 1098;
Best Local Similarity 50.3%; Pred. No. 68;
RESULT 645
ID AAS75108 standard; cDNA; 1921 BP.
DE DNA encoding novel human diagnostic protein #10912.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 32.2; DB 5; Length 1921;
Best Local Similarity 50.3%; Pred. No. 92;
RESULT 646
ID ABL17614 standard; DNA; 2501 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4315.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 32.2; DB 4; Length 2501;
Best Local Similarity 56.0%; Pred. No. 1.1e+02;
RESULT 647
ID AAH48024 standard; DNA; 14041 BP.
DE Internal control B19c #1.
PN WO200146463-A2.
PD 28-JUN-2001.
PA (BAXT) BAXTER AG.
Query Match 3.6%; Score 32.2; DB 4; Length 14041;
Best Local Similarity 15.2%; Pred. No. 2.7e+02;
RESULT 648
ID AAX53491 standard; DNA; 114955 BP.
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
PN WO9913886-A1.
PD 25-MAR-1999.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 3.6%; Score 32.2; DB 2; Length 114955;
Best Local Similarity 25.5%; Pred. No. 8.2e+02;
RESULT 649
ID ABV29078 standard; cDNA; 338 BP.
DE Human prostate expression marker cDNA 29069.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 338;
Best Local Similarity 50.7%; Pred. No. 42;
RESULT 650
ID ABV23235 standard; cDNA; 338 BP.
DE Human prostate expression marker cDNA 23226.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 338;
Best Local Similarity 50.7%; Pred. No. 42;
RESULT 651
ID ABV05108 standard; cDNA; 341 BP.
DE Human prostate expression marker cDNA 5099.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 341;
Best Local Similarity 50.7%; Pred. No. 42;
RESULT 652
ID ABV14277 standard; cDNA; 342 BP.
DE Human prostate expression marker cDNA 14268.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 342;
Best Local Similarity 50.7%; Pred. No. 42;
RESULT 653
ID ABV35370 standard; cDNA; 394 BP.
DE Human prostate expression marker cDNA 35361.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 394;
Best Local Similarity 50.7%; Pred. No. 45;
RESULT 654
ID ABV44201 standard; cDNA; 394 BP.
DE Human prostate expression marker cDNA 44192.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 394;
Best Local Similarity 50.7%; Pred. No. 45;
RESULT 655
ID ACC62613 standard; cDNA; 550 BP.
DE Rice endosperm EST #32.
PN CN1366079-A.
PD 28-AUG-2002.
PA (UYZH-) UNIV ZHEJIANG.
Query Match 3.6%; Score 32; DB 8; Length 550;
Best Local Similarity 48.4%; Pred. No. 54;
RESULT 656

ID ADL13653 standard; DNA; 1254 BP.
DE Osteoarthritis-associated polymorphic nucleotide #185.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 32; DB 10; Length 1254;
Best Local Similarity 50.7%; Pred. No. 84;
RESULT 657
ID ADL13654 standard; DNA; 1254 BP.
DE Osteoarthritis-associated polymorphic nucleotide #186.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 32; DB 10; Length 1254;
Best Local Similarity 50.7%; Pred. No. 84;
RESULT 658
ID ADI31922 standard; cDNA; 1320 BP.
DE Human cDNA #1248.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 32; DB 11; Length 1320;
Best Local Similarity 50.7%; Pred. No. 86;
RESULT 659
ID ADH13749 standard; DNA; 1325 BP.
DE Human ENZM enzyme gene sequence SeqID102.
PN WO2003093439-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 32; DB 12; Length 1325;
Best Local Similarity 50.7%; Pred. No. 87;
RESULT 660
ID AAT59298 standard; DNA; 1349 BP.
DE Human squalene synthetase coding sequence.
PN US5589372-A.
PD 31-DEC-1996.
PA (SQUI) SQUIBB & SONS INC E R.
Query Match 3.6%; Score 32; DB 2; Length 1349;
Best Local Similarity 50.7%; Pred. No. 87;
RESULT 661
ID ADJ94871 standard; DNA; 1349 BP.
DE Novel NOVX gene sequence #50.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.6%; Score 32; DB 10; Length 1349;
Best Local Similarity 50.7%; Pred. No. 87;
RESULT 662
ID ADH45327 standard; DNA; 1572 BP.
DE Human enzyme (ENZM) encoding polynucleotide, SEQ ID No 51.
PN WO2003104410-A2.
PD 18-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 32; DB 12; Length 1572;
Best Local Similarity 50.7%; Pred. No. 95;
RESULT 663
ID ACN38764 standard; cDNA; 1641 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325063, SEQ ID NO:2482.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.6%; Score 32; DB 13; Length 1641;
Best Local Similarity 50.7%; Pred. No. 97;
RESULT 664
ID ADL13659 standard; DNA; 1647 BP.
DE Osteoarthritis-associated polymorphic nucleotide #191.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 32; DB 10; Length 1647;
Best Local Similarity 50.7%; Pred. No. 97;
RESULT 665
ID ADL13652 standard; DNA; 1649 BP.
DE Osteoarthritis-associated polymorphic nucleotide #184.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 32; DB 10; Length 1649;
Best Local Similarity 50.7%; Pred. No. 97;
RESULT 666
ID ADN31611 standard; cDNA; 1649 BP.
DE Human squalene synthase cDNA #1.
PN US2004102405-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.6%; Score 32; DB 12; Length 1649;
Best Local Similarity 50.7%; Pred. No. 97;
RESULT 667
ID ADI02678 standard; cDNA; 1743 BP.
DE Human cDNA differentially expressed in the vascular endothelium #219.
PN US2003166903-A1.
PD 04-SEP-2003.
PA (ASTR/) ASTROMOFF A.
PA (BAND/) BANDMAN O.
PA (COCK/) COCKS B G.
Query Match 3.6%; Score 32; DB 10; Length 1743;
Best Local Similarity 50.7%; Pred. No. 1e+02;
RESULT 668
ID AAS80222 standard; cDNA; 1782 BP.
DE DNA encoding novel human diagnostic protein #16026.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 32; DB 5; Length 1782;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 669
ID ABV22811 standard; cDNA; 1900 BP.
DE Human prostate expression marker cDNA 22802.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 1900;
Best Local Similarity 50.7%; Pred. No. 1.1e+02;
RESULT 670
ID ABV28640 standard; cDNA; 1900 BP.
DE Human prostate expression marker cDNA 28631.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 32; DB 5; Length 1900;
Best Local Similarity 50.7%; Pred. No. 1.1e+02;
RESULT 671
ID AAQ62598 standard; DNA; 2051 BP.
DE Sequence encoding human squalene synthase.
PN GB2272442-A.
PD 18-MAY-1994.
PA (ZENE) ZENECA LTD.
Query Match 3.6%; Score 32; DB 2; Length 2051;
Best Local Similarity 50.7%; Pred. No. 1.1e+02;
RESULT 672
ID ADN31620 standard; cDNA; 2051 BP.
DE Human squalene synthase cDNA #2.
PN US2004102405-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.6%; Score 32; DB 12; Length 2051;
Best Local Similarity 50.7%; Pred. No. 1.1e+02;
RESULT 673
ID ABL30129 standard; DNA; 4428 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41860.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 32; DB 4; Length 4428;
Best Local Similarity 55.4%; Pred. No. 1.7e+02;
RESULT 674

ID ABL30128 standard; DNA; 7042 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41857.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 32; DB 4; Length 7042;
Best Local Similarity 55.4%; Pred. No. 2.1e+02;
RESULT 675
ID AAA10594 standard; DNA; 10732 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 3.6%; Score 32; DB 3; Length 10732;
Best Local Similarity 11.9%; Pred. No. 2.7e+02;
RESULT 676
ID ADF54842 standard; DNA; 96 BP.
DE Yeast VesI-1S expression system related DNA region, SEQ ID No 10.
PN JP2003284562-A.
PD 07-OCT-2003.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 3.6%; Score 31.8; DB 10; Length 96;
Best Local Similarity 61.4%; Pred. No. 24;
RESULT 677
ID ADB55356 standard; DNA; 139 BP.
DE Toxicity-related gene, SEQ ID 382.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 31.8; DB 10; Length 139;
Best Local Similarity 64.0%; Pred. No. 30;
RESULT 678
ID ADP71526 standard; DNA; 139 BP.
DE Renal toxin progression gene marker #115.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 31.8; DB 12; Length 139;
Best Local Similarity 64.0%; Pred. No. 30;
RESULT 679
ID AAC08065 standard; cDNA; 275 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 12140.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.6%; Score 31.8; DB 3; Length 275;
Best Local Similarity 51.9%; Pred. No. 43;
RESULT 680
ID ADC03371 standard; DNA; 520 BP.
DE Rice flowering time-related gene #6.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 31.8; DB 10; Length 520;
Best Local Similarity 57.6%; Pred. No. 61;
RESULT 681
ID ABD14676 standard; DNA; 528 BP.
DE Pseudomonas aeruginosa polynucleotide #13280.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 31.8; DB 11; Length 528;
Best Local Similarity 46.9%; Pred. No. 61;
RESULT 682
ID ABN62556 standard; cDNA; 568 BP.
DE Human cancer related polynucleotide SEQ ID NO 2523.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 31.8; DB 6; Length 568;
Best Local Similarity 56.1%; Pred. No. 63;
RESULT 683
ID ABD13911 standard; DNA; 780 BP.
DE Pseudomonas aeruginosa polynucleotide #12515.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 31.8; DB 11; Length 780;
Best Local Similarity 46.9%; Pred. No. 75;
RESULT 684
ID AAH47067 standard; DNA; 1020 BP.
DE Human alpha4GlcNAc-transferase encoding DNA.
PN WO200159079-A1.
PD 16-AUG-2001.
PA (CLAU/) CLAUSEN H.
Query Match 3.6%; Score 31.8; DB 4; Length 1020;
Best Local Similarity 59.3%; Pred. No. 87;
RESULT 685
ID ABZ83463 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #622.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.6%; Score 31.8; DB 10; Length 1024;
Best Local Similarity 56.1%; Pred. No. 87;
RESULT 686
ID AAK52594 standard; cDNA; 1221 BP.
DE Human polynucleotide SEQ ID NO 2123.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 31.8; DB 4; Length 1221;
Best Local Similarity 59.3%; Pred. No. 96;
RESULT 687
ID AAK51610 standard; cDNA; 1281 BP.
DE Human polynucleotide SEQ ID NO 155.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 31.8; DB 4; Length 1281;
Best Local Similarity 59.3%; Pred. No. 98;
RESULT 688
ID AAS20119 standard; cDNA; 2015 BP.
DE Human cDNA encoding cancer antigen ATF4/CREB-2.
PN WO200192306-A2.
PD 06-DEC-2001.
PA (GENZ) GENZYME CORP.
Query Match 3.6%; Score 31.8; DB 6; Length 2015;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 689
ID ACA90234 standard; cDNA; 2015 BP.
DE Deatch associated protein kinase 3 (DAPK3) interacting cDNA #6.
PN WO2003031571-A2.
PD 17-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.6%; Score 31.8; DB 8; Length 2015;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 690
ID ACC85022 standard; cDNA; 2015 BP.
DE Human cancer antigen ATF4/CREB-2 encoding cDNA.
PN WO2003050307-A1.
PD 19-JUN-2003.
PA (GENZ) GENZYME CORP.
Query Match 3.6%; Score 31.8; DB 9; Length 2015;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 691
ID ADE84922 standard; DNA; 2015 BP.
DE Farnesyl transferase inhibitor modulated leukemia associated gene #141.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 3.6%; Score 31.8; DB 10; Length 2015;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 692

ID ADF76966 standard; cDNA; 2015 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 641.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 3.6%; Score 31.8; DB 10; Length 2015;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 693
ID ADF45489 standard; cDNA; 2015 BP.
DE Human ATF4 nucleotide sequence.
PN WO2003102587-A1.
PD 11-DEC-2003.
PA (UYED-) UNIV EDINBURGH.
Query Match 3.6%; Score 31.8; DB 12; Length 2015;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 694
ID ADR24786 standard; DNA; 2015 BP.
DE Breast cancer prognosis marker #647.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 3.6%; Score 31.8; DB 13; Length 2015;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 695
ID ADE77008 standard; cDNA; 2019 BP.
DE Human cDNA differentially expressed in a liver disorder #126.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 3.6%; Score 31.8; DB 12; Length 2019;
Best Local Similarity 56.1%; Pred. No. 1.3e+02;
RESULT 696
ID ADM01515 standard; cDNA; 2490 BP.
DE Human cDNA of the invention SEQ ID NO:200.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 31.8; DB 11; Length 2490;
Best Local Similarity 61.4%; Pred. No. 1.4e+02;
RESULT 697
ID ACN37210 standard; DNA; 30265 BP.
DE Human periodontal disease related gene IL10RB SEQ ID NO:120.
Query Match 3.6%; Score 31.8; DB 13; Length 30265;
Best Local Similarity 51.9%; Pred. No. 5.4e+02;
RESULT 698
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Query Match 3.6%; Score 31.8; DB 2; Length 49999;
Best Local Similarity 48.6%; Pred. No. 7e+02;
RESULT 699
ID ACN45142 standard; DNA; 71292 BP.
DE Human genomic sequence hCG19941.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 31.8; DB 11; Length 71292;
Best Local Similarity 50.3%; Pred. No. 8.4e+02;
RESULT 700
Query Match 3.6%; Score 31.8; DB 12; Length 110000;
Best Local Similarity 51.8%; Pred. No. 1.1e+03;
RESULT 701
ID ACH19032 standard; cDNA; 404 BP.
DE Human adult lung cDNA #35.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.6%; Score 31.6; DB 9; Length 404;
Best Local Similarity 46.4%; Pred. No. 61;
RESULT 702
ID ABN19151 standard; cDNA; 474 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:6779.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 3.6%; Score 31.6; DB 6; Length 474;
Best Local Similarity 51.4%; Pred. No. 66;
RESULT 703
ID ACH33315 standard; cDNA; 496 BP.
DE Human endothelial cell cDNA #1448.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.6%; Score 31.6; DB 9; Length 496;
Best Local Similarity 60.5%; Pred. No. 68;
RESULT 704
ID ADC03397 standard; DNA; 559 BP.
DE Rice flowering time-related gene #19.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 31.6; DB 10; Length 559;
Best Local Similarity 53.2%; Pred. No. 73;
RESULT 705
ID AAA44151 standard; cDNA; 588 BP.
DE Human secreted expressed sequence tag SEQ ID NO:726.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Query Match 3.6%; Score 31.6; DB 3; Length 588;
Best Local Similarity 60.5%; Pred. No. 75;
RESULT 706
ID ACH89554 standard; DNA; 638 BP.
DE Human genome derived single exon probe #22749.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 3.6%; Score 31.6; DB 12; Length 638;
Best Local Similarity 60.5%; Pred. No. 78;
RESULT 707
ID ABD09003 standard; DNA; 852 BP.
DE Pseudomonas aeruginosa polynucleotide #7607.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 31.6; DB 11; Length 852;
Best Local Similarity 49.4%; Pred. No. 91;
RESULT 708
ID ADM47216 standard; DNA; 1042 BP.
DE Surfactant protein-C like NOVX 12b gene.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.6%; Score 31.6; DB 11; Length 1042;
Best Local Similarity 46.4%; Pred. No. 1e+02;
RESULT 709
ID AAZ12061 standard; DNA; 1341 BP.
DE Neisseria gonorrhoeae complete ORF33 sequence.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 3.6%; Score 31.6; DB 2; Length 1341;
Best Local Similarity 50.7%; Pred. No. 1.2e+02;

RESULT 710
ID ABA06568 standard; cDNA; 1360 BP.
DE Human cDNA SEQ ID NO: 234.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 31.6; DB 4; Length 1360;
Best Local Similarity 56.9%; Pred. No. 1.2e+02;
RESULT 711
ID ABV83905 standard; cDNA; 1360 BP.
DE Human polynucleotide SEQ ID NO 234.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.6%; Score 31.6; DB 6; Length 1360;
Best Local Similarity 56.9%; Pred. No. 1.2e+02;
RESULT 712
ID ABL41401 standard; DNA; 1362 BP.
DE Recombinant thermostable tryptophanase A encoding sequence.
PN KR98078038-A.
PD 16-NOV-1998.
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
Query Match 3.6%; Score 31.6; DB 3; Length 1362;
Best Local Similarity 49.4%; Pred. No. 1.2e+02;
RESULT 713
ID AAZ45592 standard; DNA; 1874 BP.
DE Nucleotide sequence of an isopentenyl isomerase 1 (Ipi1).
PN WO9963055-A1.
PD 09-DEC-1999.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
Query Match 3.6%; Score 31.6; DB 3; Length 1874;
Best Local Similarity 50.7%; Pred. No. 1.4e+02;
RESULT 714
ID ABS71580 standard; cDNA; 1874 BP.
DE C. reinhardtii isopentenyl pyrophosphatase (IPP) isomerase, cDNA.
PN US2002102631-A1.
PD 01-AUG-2002.
PA (CUNN/) CUNNINGHAM F X.
PA (SUNZ/) SUN Z.
Query Match 3.6%; Score 31.6; DB 6; Length 1874;
Best Local Similarity 50.7%; Pred. No. 1.4e+02;
RESULT 715
ID ADB53890 standard; DNA; 1945 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4432.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 31.6; DB 10; Length 1945;
Best Local Similarity 51.4%; Pred. No. 1.4e+02;
RESULT 716
ID ABL90770 standard; cDNA; 2167 BP.
DE Human polynucleotide SEQ ID NO 1332.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 31.6; DB 6; Length 2167;
Best Local Similarity 60.5%; Pred. No. 1.5e+02;
RESULT 717
ID ABK35777 standard; cDNA; 2961 BP.
DE cDNA sequence #168 encoding novel human secreted protein.
PN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 3.6%; Score 31.6; DB 6; Length 2961;
Best Local Similarity 60.5%; Pred. No. 1.8e+02;
RESULT 718
ID AAX99860 standard; DNA; 2991 BP.
DE Human secreted protein coding sequence clone gy621_1.
PN WO9938959-A1.
PD 05-AUG-1999.
PA (GEMY) GENETICS INST INC.
Query Match 3.6%; Score 31.6; DB 2; Length 2991;
Best Local Similarity 60.5%; Pred. No. 1.8e+02;
RESULT 719
ID AAS59284 standard; cDNA; 2991 BP.
DE Human cDNA encoding a secreted protein gy621_1.
PN WO200175068-A2.
PD 11-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 3.6%; Score 31.6; DB 4; Length 2991;
Best Local Similarity 60.5%; Pred. No. 1.8e+02;
RESULT 720
ID ABA90953 standard; cDNA; 2991 BP.
DE Human polynucleotide SEQ ID NO 155.
PN US2001039335-A1.
PD 08-NOV-2001.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (AGOS/) AGOSTINO M J.
PA (STEI/) STEININGER R J.
PA (SPAU/) SPAULDING V.
PA (WONG/) WONG G G.
PA (CLAR/) CLARK H.
PA (FECH/) FECHTEL K.
Query Match 3.6%; Score 31.6; DB 6; Length 2991;
Best Local Similarity 60.5%; Pred. No. 1.8e+02;
RESULT 721
ID ADB58154 standard; DNA; 3335 BP.
DE Toxicity-related gene, SEQ ID 3180.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 31.6; DB 10; Length 3335;
Best Local Similarity 48.4%; Pred. No. 1.9e+02;
RESULT 722
ID ADB52641 standard; DNA; 3335 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3183.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 31.6; DB 10; Length 3335;
Best Local Similarity 48.4%; Pred. No. 1.9e+02;
RESULT 723
ID ABT41871 standard; DNA; 3335 BP.
DE Toxicity modelling related rat gene SEQ ID No 1573.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 31.6; DB 10; Length 3335;
Best Local Similarity 48.4%; Pred. No. 1.9e+02;
RESULT 724
ID AAK94386 standard; cDNA; 3462 BP.
DE Human full-length cDNA, SEQ ID NO: 3129.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.6%; Score 31.6; DB 4; Length 3462;
Best Local Similarity 60.5%; Pred. No. 1.9e+02;
RESULT 725
ID ADL31096 standard; cDNA; 3462 BP.
DE Full length human cDNA clone SeqID 3129.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 31.6; DB 12; Length 3462;
Best Local Similarity 60.5%; Pred. No. 1.9e+02;
RESULT 726
ID AAK94780 standard; cDNA; 3487 BP.
DE Human full-length cDNA, SEQ ID NO: 3882.

PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.6%; Score 31.6; DB 4; Length 3487;
Best Local Similarity 60.5%; Pred. No. 1.9e+02;
RESULT 727
ID ADL31849 standard; cDNA; 3487 BP.
DE Full length human cDNA clone SeqID 3882.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 31.6; DB 12; Length 3487;
Best Local Similarity 60.5%; Pred. No. 1.9e+02;
RESULT 728
ID ADM03006 standard; cDNA; 3843 BP.
DE Human cDNA of the invention SEQ ID NO:1691.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 31.6; DB 11; Length 3843;
Best Local Similarity 60.5%; Pred. No. 2e+02;
RESULT 729
ID AAA53920 standard; cDNA; 4533 BP.
DE Type III adenylyl cyclase coding sequence.
PN US6107076-A.
PD 22-AUG-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 3.6%; Score 31.6; DB 3; Length 4533;
Best Local Similarity 55.5%; Pred. No. 2.2e+02;
RESULT 730
ID ADQ19293 standard; DNA; 6949 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2112.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 31.6; DB 12; Length 6949;
Best Local Similarity 60.5%; Pred. No. 2.8e+02;
RESULT 731
ID ADQ83889 standard; cDNA; 6952 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #703.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.6%; Score 31.6; DB 12; Length 6952;
Best Local Similarity 60.5%; Pred. No. 2.8e+02;
RESULT 732
ID ADQ83208 standard; cDNA; 6952 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #22.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.6%; Score 31.6; DB 12; Length 6952;
Best Local Similarity 60.5%; Pred. No. 2.8e+02;
RESULT 733
ID ADQ86306 standard; cDNA; 6952 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3178.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.6%; Score 31.6; DB 12; Length 6952;
Best Local Similarity 60.5%; Pred. No. 2.8e+02;
RESULT 734
ID ADQ84377 standard; cDNA; 6952 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1191.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.6%; Score 31.6; DB 12; Length 6952;
Best Local Similarity 60.5%; Pred. No. 2.8e+02;
RESULT 735
ID ADQ85117 standard; cDNA; 6952 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1931.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.6%; Score 31.6; DB 13; Length 6952;
Best Local Similarity 60.5%; Pred. No. 2.8e+02;
RESULT 736
ID ADQ23558 standard; DNA; 7066 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6378.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 31.6; DB 12; Length 7066;
Best Local Similarity 60.5%; Pred. No. 2.8e+02;
RESULT 737
ID ABL12715 standard; cDNA; 7395 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32627.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 31.6; DB 4; Length 7395;
Best Local Similarity 49.4%; Pred. No. 2.9e+02;
RESULT 738
ID AAK73225 standard; DNA; 9359 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28037.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 31.6; DB 4; Length 9359;
Best Local Similarity 47.9%; Pred. No. 3.3e+02;
RESULT 739
ID ABK84514 standard; cDNA; 12263 BP.
DE Human cDNA differentially expressed in granulocytic cells #1085.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 31.6; DB 6; Length 12263;
Best Local Similarity 54.2%; Pred. No. 3.8e+02;
RESULT 740
ID ABA94501 standard; DNA; 15297 BP.
DE Human proto-oncogene tyrosine kinase genomic DNA sequence.
PN US6340584-B1.
PD 22-JAN-2002.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 31.6; DB 6; Length 15297;
Best Local Similarity 54.2%; Pred. No. 4.3e+02;
RESULT 741
ID ABV75414 standard; DNA; 15297 BP.
DE Human kinase genomic DNA sequence.
PN WO200277191-A2.
PD 03-OCT-2002.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 31.6; DB 8; Length 15297;
Best Local Similarity 54.2%; Pred. No. 4.3e+02;
RESULT 742
ID ADM28582 standard; cDNA; 15297 BP.
DE Human proto-oncogene tyrosine kinase DNA.
PN US2004063130-A1.
PD 01-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.6%; Score 31.6; DB 12; Length 15297;
Best Local Similarity 54.2%; Pred. No. 4.3e+02;
RESULT 743
ID AAA58472 standard; DNA; 18660 BP.
DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.

PN WO200040704-A1.
PD 13-JUL-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 3.6%; Score 31.6; DB 3; Length 18660;
Best Local Similarity 62.8%; Pred. No. 4.8e+02;
RESULT 744
ID ABL12714 standard; cDNA; 20604 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32624.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 31.6; DB 4; Length 20604;
Best Local Similarity 49.4%; Pred. No. 5e+02;
RESULT 745
ID AAS34624 standard; DNA; 27289 BP.
DE Human DNA for a novel foetal antigen, SEQ ID No 2048.
PN WO200155312-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 31.6; DB 5; Length 27289;
Best Local Similarity 60.5%; Pred. No. 5.9e+02;
RESULT 746
ID ABA16117 standard; DNA; 32186 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8448.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 31.6; DB 5; Length 32186;
Best Local Similarity 60.5%; Pred. No. 6.4e+02;
RESULT 747
ID ADC87424 standard; DNA; 34551 BP.
DE Human GPCR gene SEQ ID NO:1877.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.6%; Score 31.6; DB 10; Length 34551;
Best Local Similarity 55.5%; Pred. No. 6.6e+02;
RESULT 748
ID AAK81745 standard; DNA; 46553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36557.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 31.6; DB 4; Length 46553;
Best Local Similarity 60.5%; Pred. No. 7.8e+02;
RESULT 749
ID AAK67926 standard; DNA; 46553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22738.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 31.6; DB 4; Length 46553;
Best Local Similarity 60.5%; Pred. No. 7.8e+02;
RESULT 750
ID ACN43954 standard; DNA; 95683 BP.
DE Human genomic sequence hCG37570.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 31.6; DB 11; Length 95683;
Best Local Similarity 52.2%; Pred. No. 1.1e+03;
RESULT 751
ID ADC85260 standard; DNA; 96588 BP.
DE Human Ptprk genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 31.6; DB 10; Length 96588;
Best Local Similarity 56.9%; Pred. No. 1.1e+03;
RESULT 752
ID ADA02780 standard; DNA; 96589 BP.
DE Human PTPRK carcinoma associated gene, SEQ ID NO:1298.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 31.6; DB 9; Length 96589;
Best Local Similarity 56.9%; Pred. No. 1.1e+03;
RESULT 753
ID ADB72518 standard; DNA; 96589 BP.
DE Human PTPRK gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 31.6; DB 10; Length 96589;
Best Local Similarity 56.9%; Pred. No. 1.1e+03;
RESULT 754
ID ADM74375 standard; DNA; 96589 BP.
DE Human carcinoma associated (CA) nucleic acid #22.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 3.6%; Score 31.6; DB 12; Length 96589;
Best Local Similarity 56.9%; Pred. No. 1.1e+03;
RESULT 755
ID ACN45090 standard; DNA; 350764 BP.
DE Human genomic sequence hCG22125.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 31.6; DB 11; Length 110000;
Best Local Similarity 47.5%; Pred. No. 1.2e+03;
RESULT 756
ID ADL13501 standard; DNA; 167932 BP.
DE Osteoarthritis-associated polymorphic nucleotide #33.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 31.6; DB 10; Length 167932;
Best Local Similarity 60.5%; Pred. No. 1.5e+03;
RESULT 757
ID ABX87574 standard; cDNA; 303 BP.
DE Corn ear-derived polynucleotide (cpd) #6034.
PN US6476212-B1.
PD 05-NOV-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.5%; Score 31.4; DB 10; Length 303;
Best Local Similarity 44.8%; Pred. No. 60;
RESULT 758
ID AAC90668 standard; cDNA; 519 BP.
DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 43.
PN WO200071722-A1.
PD 30-NOV-2000.
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
Query Match 3.5%; Score 31.4; DB 4; Length 519;
Best Local Similarity 51.8%; Pred. No. 81;
RESULT 759
ID ADR14918 standard; cDNA; 519 BP.
DE Rosa sp flower bud formation suppressor encoding cDNA SEQ ID NO:1.
PN WO2004070036-A1.
PD 19-AUG-2004.
PA (WAKT) WAKUNAGA PHARM CO LTD.
Query Match 3.5%; Score 31.4; DB 13; Length 519;
Best Local Similarity 51.8%; Pred. No. 81;
RESULT 760
ID AAD50774 standard; DNA; 535 BP.
DE Clone-B29 DNA used to illustrate the method of the invention.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.5%; Score 31.4; DB 8; Length 535;
Best Local Similarity 48.6%; Pred. No. 82;
RESULT 761
ID ABQ91072 standard; DNA; 717 BP.

DE M. capsulatus gene #1057 for DNA array.
PN WO200255655-A2.
PD 18-JUL-2002.
PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
PA (TIGR-) TIGR.
Query Match 3.5%; Score 31.4; DB 6; Length 717;
Best Local Similarity 54.9%; Pred. No. 96;
RESULT 762
ID AAF17574 standard; cDNA; 750 BP.
DE Human breast cancer associated SYN22B4 coding sequence.
PN WO200060076-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.4; DB 4; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 763
ID AAS47004 standard; cDNA; 750 BP.
DE Human breast cancer cDNA clone SYN22B4.
PN WO200179286-A2.
PD 25-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.4; DB 4; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 764
ID ABK95040 standard; cDNA; 750 BP.
DE Human breast tumour cDNA SYN22B4.
PN US6387697-B1.
PD 14-MAY-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.4; DB 6; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 765
ID ABT08659 standard; cDNA; 750 BP.
DE Human breast antigen-related nucleotide #58.
PN US2002102602-A1.
PD 01-AUG-2002.
PA (YUQI/) YUQIU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (XUJJ/) XU J.
Query Match 3.5%; Score 31.4; DB 6; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 766
ID ABS63605 standard; cDNA; 750 BP.
DE Human breast tumour polynucleotide #58.
PN US2002085998-A1.
PD 04-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.4; DB 6; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 767
ID ABT32817 standard; DNA; 750 BP.
DE Human tumour-related DNA sequence - SEQ ID No 58.
PN WO200283956-A1.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.4; DB 10; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 768
ID ADL92720 standard; cDNA; 750 BP.
DE Human breast cancer-associated polypeptide cDNA #58.
PN US2003166022-A1.
PD 04-SEP-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.4; DB 11; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 769
ID ADE44489 standard; cDNA; 750 BP.
DE Human cDNA associated with breast cancer #58.
PN US2003104366-A1.
PD 05-JUN-2003.
PA (JIAN/) JIANG Y.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (XUJJ/) XU J.
PA (HARL/) HARLOCKER S L.
Query Match 3.5%; Score 31.4; DB 12; Length 750;
Best Local Similarity 53.7%; Pred. No. 98;
RESULT 770
ID AAD42254 standard; cDNA; 836 BP.
DE Soybean FT homologue cDNA #2.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 31.4; DB 6; Length 836;
Best Local Similarity 51.8%; Pred. No. 1e+02;
RESULT 771
ID ADR04272 standard; cDNA; 836 BP.
DE Soybean FT homologue encoding cDNA SEQ ID NO:39.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 31.4; DB 13; Length 836;
Best Local Similarity 51.8%; Pred. No. 1e+02;
RESULT 772
ID AAA76284 standard; cDNA; 1074 BP.
DE Maize glutathione-S-transferase coding sequence fragment SEQ ID NO: 67.
PN US6096504-A.
PD 01-AUG-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 31.4; DB 3; Length 1074;
Best Local Similarity 47.3%; Pred. No. 1.2e+02;
RESULT 773
ID ADB87378 standard; DNA; 1246 BP.
DE Transgene expression regulatory element, STAR23.
PN WO2003004704-A2.
PD 16-JAN-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 3.5%; Score 31.4; DB 10; Length 1246;
Best Local Similarity 50.3%; Pred. No. 1.3e+02;
RESULT 774
ID ADJ35187 standard; DNA; 1246 BP.
DE Human stabilising anti-repression, STAR, element #23.
PN WO2003106674-A2.
PD 24-DEC-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 3.5%; Score 31.4; DB 12; Length 1246;
Best Local Similarity 50.3%; Pred. No. 1.3e+02;
RESULT 775
ID ADL96805 standard; DNA; 1246 BP.
DE STablizing Anti-Repressor DNA sequence, STAR 23.
PN WO2003106684-A2.
PD 24-DEC-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 3.5%; Score 31.4; DB 12; Length 1246;
Best Local Similarity 50.3%; Pred. No. 1.3e+02;
RESULT 776
ID ADT43932 standard; cDNA; 1437 BP.
DE Bacterial polynucleotide #18683.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.5%; Score 31.4; DB 13; Length 1437;
Best Local Similarity 54.9%; Pred. No. 1.4e+02;
RESULT 777
ID ABD03443 standard; DNA; 2163 BP.
DE Pseudomonas aeruginosa polynucleotide #2047.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 31.4; DB 11; Length 2163;

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  Best Local Similarity   46.5%;  Pred. No. 1.7e+02;
RESULT 778
ID   ACA54650 standard; cDNA; 2729 BP.
DE   Human NF-kappaB associated polynucleotide sequence #90.
PN   WO200286076-A2.
PD   31-OCT-2002.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             3.5%;  Score 31.4;  DB 10;  Length 2729;
  Best Local Similarity   57.7%;  Pred. No. 2e+02;
RESULT 779
ID   AAH17410 standard; cDNA; 2893 BP.
DE   Human cDNA sequence SEQ ID NO:16851.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
  Query Match             3.5%;  Score 31.4;  DB 4;  Length 2893;
  Best Local Similarity   57.7%;  Pred. No. 2e+02;
RESULT 780
ID   ADR14676 standard; DNA; 2893 BP.
DE   Human NF-kappaB pathway-associated gene SeqID747.
PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             3.5%;  Score 31.4;  DB 13;  Length 2893;
  Best Local Similarity   57.7%;  Pred. No. 2e+02;
RESULT 781
ID   ACA54621 standard; cDNA; 2906 BP.
DE   Human NF-kappaB associated polynucleotide sequence #61.
PN   WO200286076-A2.
PD   31-OCT-2002.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             3.5%;  Score 31.4;  DB 10;  Length 2906;
  Best Local Similarity   57.7%;  Pred. No. 2e+02;
RESULT 782
ID   ABD03305 standard; DNA; 3546 BP.
DE   Pseudomonas aeruginosa polynucleotide #1909.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.5%;  Score 31.4;  DB 11;  Length 3546;
  Best Local Similarity   46.5%;  Pred. No. 2.3e+02;
RESULT 783
ID   AAS59522 standard; DNA; 37286 BP.
DE   Propionibacterium acnes immunogenic protein encoding DNA #17.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
  Query Match             3.5%;  Score 31.4;  DB 4;  Length 37286;
  Best Local Similarity   51.0%;  Pred. No. 8e+02;
RESULT 784
ID   ACF64451 standard; DNA; 37286 BP.
DE   Propionibacterium acnes DNA contig sequence #17.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
  Query Match             3.5%;  Score 31.4;  DB 8;  Length 37286;
  Best Local Similarity   51.0%;  Pred. No. 8e+02;
RESULT 785
ID   ACA64895 standard; DNA; 134292 BP.
DE   Human GABBR1 DNA corresponding to AL031983.
PN   DE10127572-A1.
PD   05-DEC-2002.
PA   (PATH-) PATHOARRAY GMBH.
  Query Match             3.5%;  Score 31.4;  DB 8;  Length 134292;
  Best Local Similarity   49.7%;  Pred. No. 1.6e+03;
RESULT 786
ID   ACH25503 standard; cDNA; 442 BP.
DE   Human adult ovary cDNA #3883.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.5%;  Score 31.2;  DB 9;  Length 442;
  Best Local Similarity   57.0%;  Pred. No. 85;
RESULT 787
ID   ACH23976 standard; cDNA; 457 BP.
DE   Human adult ovary cDNA #2356.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.5%;  Score 31.2;  DB 9;  Length 457;
  Best Local Similarity   57.0%;  Pred. No. 87;
RESULT 788
ID   ACH23193 standard; cDNA; 461 BP.
DE   Human adult ovary cDNA #1573.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.5%;  Score 31.2;  DB 9;  Length 461;
  Best Local Similarity   57.0%;  Pred. No. 87;
RESULT 789
ID   ADC25964 standard; cDNA; 1437 BP.
DE   Grape UDP-glucosyltransferase cDNA.
PN   WO2003066836-A2.
PD   14-AUG-2003.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
  Query Match             3.5%;  Score 31.2;  DB 10;  Length 1437;
  Best Local Similarity   58.7%;  Pred. No. 1.6e+02;
RESULT 790
ID   AAS59775 standard; DNA; 1441 BP.
DE   Propionibacterium acnes immunogenic protein encoding DNA #270.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
  Query Match             3.5%;  Score 31.2;  DB 4;  Length 1441;
  Best Local Similarity   54.3%;  Pred. No. 1.6e+02;
RESULT 791
ID   ACF64704 standard; DNA; 1441 BP.
DE   Propionibacterium acnes DNA contig sequence #270.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
  Query Match             3.5%;  Score 31.2;  DB 8;  Length 1441;
  Best Local Similarity   54.3%;  Pred. No. 1.6e+02;
RESULT 792
ID   ABD13948 standard; DNA; 1527 BP.
DE   Pseudomonas aeruginosa polynucleotide #12552.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.5%;  Score 31.2;  DB 11;  Length 1527;
  Best Local Similarity   44.6%;  Pred. No. 1.7e+02;
RESULT 793
ID   ABD14328 standard; DNA; 2022 BP.
DE   Pseudomonas aeruginosa polynucleotide #12932.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.5%;  Score 31.2;  DB 11;  Length 2022;
  Best Local Similarity   44.6%;  Pred. No. 1.9e+02;
RESULT 794
ID   ADQ97213 standard; DNA; 3500 BP.
DE   Mouse cancer associated sequence MR08-014, SEQ ID 189.
PN   WO2004060304-A2.
PD   22-JUL-2004.
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PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 31.2; DB 12; Length 3500;
Best Local Similarity 60.7%; Pred. No. 2.6e+02;
RESULT 795
ID ABL09085 standard; cDNA; 3814 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21737.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 31.2; DB 4; Length 3814;
Best Local Similarity 48.8%; Pred. No. 2.7e+02;
RESULT 796
ID ABL09084 standard; cDNA; 5993 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21734.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 31.2; DB 4; Length 5993;
Best Local Similarity 48.8%; Pred. No. 3.5e+02;
RESULT 797
ID AAK86476 standard; DNA; 27804 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41288.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 31.2; DB 4; Length 27804;
Best Local Similarity 51.4%; Pred. No. 7.9e+02;
RESULT 798
ID AAS59609 standard; DNA; 29112 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #104.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.2; DB 4; Length 29112;
Best Local Similarity 54.3%; Pred. No. 8.1e+02;
RESULT 799
ID ACF64538 standard; DNA; 29112 BP.
DE Propionibacterium acnes DNA contig sequence #104.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 31.2; DB 8; Length 29112;
Best Local Similarity 54.3%; Pred. No. 8.1e+02;
RESULT 800
ID ADQ97212 standard; DNA; 50833 BP.
DE Mouse cancer associated sequence MD08-014, SEQ ID 188.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 31.2; DB 12; Length 50833;
Best Local Similarity 60.7%; Pred. No. 1.1e+03;
RESULT 801
ID ACN44074 standard; DNA; 128668 BP.
DE Human genomic sequence hCG40471.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 31.2; DB 11; Length 128668;
Best Local Similarity 51.4%; Pred. No. 1.8e+03;
RESULT 802
ID ADL08124 standard; DNA; 176080 BP.
DE Human gene associated with low HDL-C LRPAP1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 3.5%; Score 31.2; DB 12; Length 176080;
Best Local Similarity 57.0%; Pred. No. 2.1e+03;
RESULT 803
ID AAC84906 standard; DNA; 31 BP.
DE Probe Ag 36 (P) employed in expression analysis of SEC1 (3445452).
PN WO200078802-A2.
PD 28-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match 3.5%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 24;
RESULT 804
ID ADG76241 standard; DNA; 31 BP.
DE Labelled DNA oligo probe used to isolate NOVX DNA SeqID154.
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.5%; Score 31; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 24;
RESULT 805
ID ADK68297 standard; DNA; 31 BP.
DE Novel NOVX gene probe #20.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.5%; Score 31; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 24;
RESULT 806
ID ADR49286 standard; DNA; 31 BP.
DE Human NOV8 probe Ag36.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 3.5%; Score 31; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 24;
RESULT 807
ID ABD04322 standard; DNA; 264 BP.
DE Pseudomonas aeruginosa polynucleotide #2926.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 31; DB 11; Length 264;
Best Local Similarity 57.9%; Pred. No. 75;
RESULT 808
ID AAI83100 standard; cDNA; 378 BP.
DE Human polynucleotide SEQ ID NO 3160.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 31; DB 4; Length 378;
Best Local Similarity 72.7%; Pred. No. 91;
RESULT 809
ID ACH27120 standard; cDNA; 407 BP.
DE Human adult ovary cDNA #5500.

PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.5%; Score 31; DB 9; Length 407;
Best Local Similarity 56.3%; Pred. No. 94;
RESULT 810
ID ACH40713 standard; cDNA; 468 BP.
DE Human foetal brain cDNA #2080.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.5%; Score 31; DB 9; Length 468;
Best Local Similarity 52.8%; Pred. No. 1e+02;
RESULT 811
ID ADA01712 standard; DNA; 529 BP.
DE Mouse Saas carcinoma associated nucleic acid, SEQ ID NO:231.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 31; DB 9; Length 529;
Best Local Similarity 62.0%; Pred. No. 1.1e+02;
RESULT 812
ID ADB71451 standard; DNA; 529 BP.
DE Mouse carcinoma associated gene fragment #231.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 31; DB 10; Length 529;
Best Local Similarity 62.0%; Pred. No. 1.1e+02;
RESULT 813
ID ABL12203 standard; cDNA; 766 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31091.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 31; DB 4; Length 766;
Best Local Similarity 50.2%; Pred. No. 1.3e+02;
RESULT 814
ID AAD42255 standard; cDNA; 893 BP.
DE Wheat FT homologue cDNA from clone wdk2c.pk012.017.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 31; DB 6; Length 893;
Best Local Similarity 57.9%; Pred. No. 1.4e+02;
RESULT 815
ID ADR04274 standard; cDNA; 893 BP.
DE Wheat FT homologue encoding cDNA SEQ ID NO:41.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 31; DB 13; Length 893;
Best Local Similarity 57.9%; Pred. No. 1.4e+02;
RESULT 816
ID ADN74883 standard; cDNA; 1140 BP.
DE Rice RCN2 cDNA used to delay the flowering stage of the plant SeqID 3.
PN JP2004089026-A.
PD 25-MAR-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 3.5%; Score 31; DB 12; Length 1140;
Best Local Similarity 52.8%; Pred. No. 1.6e+02;
RESULT 817
ID AAD42250 standard; cDNA; 1295 BP.
DE Rice FT homologue cDNA from clone rr1.pk0043.f9.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 31; DB 6; Length 1295;
Best Local Similarity 52.8%; Pred. No. 1.8e+02;
RESULT 818
ID ADR04264 standard; cDNA; 1295 BP.
DE Rice FT homologue encoding cDNA SEQ ID NO:31.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 31; DB 13; Length 1295;
Best Local Similarity 52.8%; Pred. No. 1.8e+02;
RESULT 819
ID AAV34599 standard; DNA; 1341 BP.
DE M. vaccae potD homologue encoding DNA.
PN WO9808542-A2.
PD 05-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP.
Query Match 3.5%; Score 31; DB 2; Length 1341;
Best Local Similarity 48.6%; Pred. No. 1.8e+02;
RESULT 820
ID AAZ11334 standard; DNA; 1341 BP.
DE M. vaccae potd gene homologue nucleotide sequence.
PN WO9932634-A2.
PD 01-JUL-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 3.5%; Score 31; DB 2; Length 1341;
Best Local Similarity 48.6%; Pred. No. 1.8e+02;
RESULT 821
ID ABL36240 standard; DNA; 1341 BP.
DE M vaccae potd coding sequence SEQ ID NO: 93.
PN US6328978-B1.
PD 11-DEC-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 3.5%; Score 31; DB 6; Length 1341;
Best Local Similarity 48.6%; Pred. No. 1.8e+02;
RESULT 822
ID ADA21197 standard; cDNA; 1548 BP.
DE Human secreted protein SECP-51 encoding cDNA SEQ ID NO:102.
PN WO2003068943-A2.
PD 21-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.5%; Score 31; DB 9; Length 1548;
Best Local Similarity 62.0%; Pred. No. 1.9e+02;
RESULT 823
ID AAS64702 standard; cDNA; 1578 BP.
DE DNA encoding novel human diagnostic protein #506.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 31; DB 5; Length 1578;
Best Local Similarity 62.0%; Pred. No. 2e+02;
RESULT 824
ID AAD54301 standard; cDNA; 1699 BP.
DE Human SECP-15 cDNA.
PN WO200297035-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.5%; Score 31; DB 10; Length 1699;
Best Local Similarity 62.0%; Pred. No. 2e+02;
RESULT 825
ID ADC27724 standard; DNA; 1783 BP.
DE Human colon specific nucleic acid (CSNA) Seq ID93.
PN WO2003020953-A2.
PD 13-MAR-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 3.5%; Score 31; DB 10; Length 1783;
Best Local Similarity 62.0%; Pred. No. 2.1e+02;
RESULT 826
ID ADD69653 standard; cDNA; 1788 BP.
DE Human REMAP cDNA - SEQ ID 82.

PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.5%; Score 31; DB 10; Length 1788;
Best Local Similarity 50.3%; Pred. No. 2.1e+02;
RESULT 827
ID AAC69090 standard; DNA; 2178 BP.
DE Human secreted protein gene 7 clone HWLHH15.
PN WO200055371-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 31; DB 3; Length 2178;
Best Local Similarity 62.0%; Pred. No. 2.3e+02;
RESULT 828
ID ABD17163 standard; DNA; 2502 BP.
DE Pseudomonas aeruginosa polynucleotide #15767.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 31; DB 11; Length 2502;
Best Local Similarity 47.2%; Pred. No. 2.5e+02;
RESULT 829
ID ADB63219 standard; cDNA; 2581 BP.
DE Human cDNA encoding clone SPLEN20190770.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.5%; Score 31; DB 10; Length 2581;
Best Local Similarity 62.0%; Pred. No. 2.5e+02;
RESULT 830
ID ADB58098 standard; DNA; 2599 BP.
DE Toxicity-related gene, SEQ ID 3124.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 31; DB 10; Length 2599;
Best Local Similarity 49.1%; Pred. No. 2.5e+02;
RESULT 831
ID ADB52579 standard; DNA; 2599 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3121.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 31; DB 10; Length 2599;
Best Local Similarity 49.1%; Pred. No. 2.5e+02;
RESULT 832
ID AAN90750 standard; DNA; 2600 BP.
DE Protein kinase C beta 1 cDNA.
PN WO8907654-A.
PD 24-AUG-1989.
PA (PROG-) PROGENICS PHARM INC.
PA (HOUS/) HOUSEY G M.
PA (HOUS/) HOUSEY G M.
Query Match 3.5%; Score 31; DB 1; Length 2600;
Best Local Similarity 49.1%; Pred. No. 2.6e+02;
RESULT 833
ID AAK94141 standard; cDNA; 2994 BP.
DE Human full-length cDNA, SEQ ID NO: 2650.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.5%; Score 31; DB 4; Length 2994;
Best Local Similarity 52.8%; Pred. No. 2.8e+02;
RESULT 834
ID ADL30617 standard; cDNA; 2994 BP.
DE Full length human cDNA clone SeqID 2650.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.5%; Score 31; DB 12; Length 2994;
Best Local Similarity 52.8%; Pred. No. 2.8e+02;
RESULT 835
ID ADP28247 standard; DNA; 3018 BP.
DE Human secreted protein encoding sequence SEQ ID #245.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 3.5%; Score 31; DB 12; Length 3018;
Best Local Similarity 52.8%; Pred. No. 2.8e+02;
RESULT 836
ID ADP28237 standard; DNA; 3018 BP.
DE Human secreted protein encoding sequence SEQ ID #235.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 3.5%; Score 31; DB 12; Length 3018;
Best Local Similarity 52.8%; Pred. No. 2.8e+02;
RESULT 837
ID ADJ92164 standard; cDNA; 3078 BP.
DE Human hair keratin-associated-protein encoding cDNA SEQ ID NO:23.
PN WO2003042387-A1.
PD 22-MAY-2003.
PA (UYKE-) UNIV KEIO.
PA (NIPR-) JAPAN SOC PROMOTION SCI.
Query Match 3.5%; Score 31; DB 10; Length 3078;
Best Local Similarity 56.3%; Pred. No. 2.8e+02;
RESULT 838
ID AAH16265 standard; cDNA; 3384 BP.
DE Human cDNA sequence SEQ ID NO:15117.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.5%; Score 31; DB 4; Length 3384;
Best Local Similarity 51.9%; Pred. No. 2.9e+02;
RESULT 839
ID ADM12939 standard; cDNA; 3534 BP.
DE PRO83473 encoding sequence.
PN WO2004024077-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 3534;
Best Local Similarity 52.8%; Pred. No. 3e+02;
RESULT 840
ID ADN05141 standard; cDNA; 3534 BP.
DE Antipsoriatic cDNA sequence #786.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 3534;
Best Local Similarity 52.8%; Pred. No. 3e+02;
RESULT 841
ID AAS01215 standard; cDNA; 3550 BP.
DE DNA encoding human secreted protein, POLY6.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 3.5%; Score 31; DB 5; Length 3550;
Best Local Similarity 52.8%; Pred. No. 3e+02;
RESULT 842
ID ADH89013 standard; cDNA; 3550 BP.
DE Human POLYX polynucleotide #6.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LIUX/) LIU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 3.5%; Score 31; DB 12; Length 3550;
Best Local Similarity 52.8%; Pred. No. 3e+02;
RESULT 843
ID ADD89097 standard; cDNA; 3636 BP.

DE Encoding sequence TAT262.
PN WO2003057160-A2.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 3636;
Best Local Similarity 56.3%; Pred. No. 3.1e+02;
RESULT 844
ID ABD17192 standard; DNA; 4257 BP.
DE Pseudomonas aeruginosa polynucleotide #15796.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 31; DB 11; Length 4257;
Best Local Similarity 47.2%; Pred. No. 3.3e+02;
RESULT 845
ID AAA37039 standard; cDNA; 4277 BP.
DE Human PRO1190 (UNQ604) cDNA sequence SEQ ID NO:57.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 3; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 846
ID AAF54241 standard; DNA; 4277 BP.
DE DNA encoding protein of the invention #18.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 4; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 847
ID AAS46144 standard; cDNA; 4277 BP.
DE Human DNA encoding PRO polypeptide sequence #220.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 4; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 848
ID ABL88150 standard; cDNA; 4277 BP.
DE Human PRO1190 cDNA sequence SEQ ID NO:157.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 6; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 849
ID ABL95639 standard; cDNA; 4277 BP.
DE Human angiogenesis related cDNA PRO1190 SEQ ID NO: 157.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 3.5%; Score 31; DB 6; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 850
ID ACA89594 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 851
ID ACA73604 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 852
ID ACA05919 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 853
ID ACA66753 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO protein #220.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 854
ID ACF20328 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 855
ID ACF19714 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 856
ID ACD22002 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 857
ID ACF13167 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 858
ID ACD25270 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 859
ID ACF00319 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 860
ID ACA72376 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.

PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 861
ID ACD04900 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 862
ID ACD18361 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 863
ID ACD08368 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 864
ID ACA88802 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 865
ID ACA70244 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 866
ID ACD12466 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 867
ID ACC74381 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 868
ID ACD16009 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 869
ID ACD25577 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 870
ID ACD18054 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 871
ID ACC88341 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 872
ID ACD21695 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 873
ID ACD18762 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 874
ID ABX98372 standard; cDNA; 4277 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 439.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 875
ID ACD14123 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 876
ID ACD09903 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 877
ID ACC88648 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 878
ID ACD21388 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 879
ID ABX75760 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1190.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 880
ID ABX97963 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;

RESULT 881
ID ACA97439 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 882
ID ACA57902 standard; cDNA; 4277 BP.
DE Human PRO1190 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 883
ID ACD14430 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 884
ID ACC91213 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 885
ID ACC88955 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 886
ID ACD07152 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 887
ID ACA67603 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 888
ID ACC81658 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 889
ID ACC89262 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 890
ID ACC86618 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 891
ID ACC89876 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 892
ID ACC93055 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 893
ID ACA72683 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 894
ID ACA89201 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 895
ID ACA69937 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 896
ID ACA97080 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 897
ID ACA91076 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 898
ID ACA70858 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 899
ID ACA95368 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 900
ID ACC86311 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 901
ID ACC90183 standard; cDNA; 4277 BP.

DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 902
ID ACD12791 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 903
ID ACF20021 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 904
ID ABX76965 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 905
ID ACA73297 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 906
ID ACA68840 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 907
ID ACA74684 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 908
ID ACA70551 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 909
ID ACD14737 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 910
ID ACA68409 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 911
ID ABX98874 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 912
ID ACC81351 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 913
ID ACA95675 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 914
ID ACD04593 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 915
ID ACC88034 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 916
ID ACF12696 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 917
ID ACA96411 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 918
ID ACA65185 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 919
ID ACA73911 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 920
ID ACA74323 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 921
ID ACA96718 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 8; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;

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RESULT 922
ID   ACD10824 standard; cDNA; 4277 BP.
DE   cDNA encoding human PRO polypeptide #220.
PN   US2003032107-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 923
ID   ACC91520 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003032139-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 924
ID   ACD02855 standard; cDNA; 4277 BP.
DE   cDNA encoding human PRO polypeptide #220.
PN   US2003022301-A1.
PD   30-JAN-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 925
ID   ACC87420 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 926
ID   ACC86004 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003027262-A1.
PD   06-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 927
ID   ACA65492 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #220.
PN   US2003032110-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 928
ID   ACA94309 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003036142-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 929
ID   ACA98053 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #220.
PN   US2003036145-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 930
ID   ACA91555 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003036154-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 931
ID   ACA90769 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003036153-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 932
ID   ACD16316 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003044931-A1.
PD   06-MAR-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 933
ID   ACD17477 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003036150-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 934
ID   ACC92134 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003040069-A1.
PD   27-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 935
ID   ACA74991 standard; cDNA; 4277 BP.
DE   cDNA encoding human PRO polypeptide #220.
PN   US2003022293-A1.
PD   30-JAN-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 936
ID   ACA91862 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #220.
PN   US2003032128-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 937
ID   ACA71506 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003032116-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 938
ID   ACC90906 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003032122-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 939
ID   ACA65916 standard; cDNA; 4277 BP.
DE   cDNA encoding human PRO protein #220.
PN   US2003036139-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 940
ID   ACA95061 standard; cDNA; 4277 BP.
DE   cDNA encoding human PRO polypeptide #220.
PN   US2003017541-A1.
PD   23-JAN-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 941
ID   ACD16623 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003017543-A1.
PD   23-JAN-2003.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 942
ID   ACD15702 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003036152-A1.
PD   20-FEB-2003.
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  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 943
ID   ABX16805 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein #220.
PN   US2002127584-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 8;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 944
ID   ACA97746 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #220.
PN   US2003032115-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 945
ID   ACA99195 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003032140-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 946
ID   ACC91827 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003040076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 947
ID   ACD11238 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003008352-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 948
ID   ACD15088 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003044922-A1.
PD   06-MAR-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 949
ID   ACD11852 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003032118-A1.
PD   13-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 950
ID   ACC95981 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003036135-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 951
ID   ACF16544 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 952
ID   ACF02662 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 953
ID   ACF02969 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 954
ID   ACF21556 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 955
ID   ACF10240 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 956
ID   ACF78133 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 957
ID   ACD46838 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 958
ID   ACD49601 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 959
ID   ACF28368 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 960
ID   ACD89058 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 961
ID   ACD84453 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #220.
PN   US2003068701-A1.
PD   10-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 962
ID ACD99227 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 963
ID ADA78191 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 964
ID ACF48969 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 965
ID ACD09289 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 966
ID ACF12082 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 967
ID ACF41316 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 968
ID ACF15930 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 969
ID ACF16237 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 970
ID ACD32064 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 971
ID ACF18872 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 972
ID ACF09319 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 973
ID ACF78440 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 974
ID ACF52039 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 975
ID ACF26526 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 976
ID ACF24319 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 977
ID ACF63630 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 978
ID ACF50504 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 979
ID ACH07975 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 980
ID ACF13781 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064462-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 981
ID ACD41707 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 982
ID ACF32120 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 983
ID ACF23398 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 984
ID ACF40088 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 985
ID ACD45610 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 986
ID ACF53267 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 987
ID ACF27447 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 988
ID ACF45285 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 989
ID ACF29903 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 990
ID ACD89979 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 991
ID ACD84760 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 992
ID ACD98920 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 993
ID ACF77212 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 994
ID ACF76905 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 995
ID ACF49890 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 996
ID ACF50197 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 997
ID ACD09596 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 998
ID ACD08675 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 999
ID ACF12389 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.

PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1000
ID ACC94897 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1001
ID ACD22616 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1002
ID ACF15316 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1003
ID ACC97411 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1004
ID ACC92441 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1005
ID ACF14088 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1006
ID ACF14395 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1007
ID ACF09626 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1008
ID ACD68278 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1009
ID ACD45917 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1010
ID ACD48066 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1011
ID ACD67797 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1012
ID ACF25605 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1013
ID ACF29289 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1014
ID ACD85067 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1015
ID ACD84146 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1016
ID ACD88137 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1017
ID ACF30824 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;

RESULT 1018
ID ACF32427 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1019
ID ACH12087 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1020
ID ACH12394 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1021
ID ACD40786 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1022
ID ACF18258 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1023
ID ACF08705 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1024
ID ACF31506 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1025
ID ACF52346 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1026
ID ACD50215 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1027
ID ACF38918 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1028
ID ACF26833 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1029
ID ACF24933 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1030
ID ACF46513 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1031
ID ACF28061 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1032
ID ACD89365 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1033
ID ACF63937 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1034
ID ACF60577 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1035
ID ACH12701 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1036
ID ACH10124 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049777-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1037
ID ACD03979 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1038
ID ACD10517 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1039
ID ACD12159 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1040
ID ACF42544 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1041
ID ACF18565 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1042
ID ACF02355 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1043
ID ACF21863 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1044
ID ACF10547 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1045
ID ACF33999 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1046
ID ACF44961 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1047
ID ACD90593 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1048
ID ACD91206 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1049
ID ACF30517 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1050
ID ACD87216 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1051
ID ACF60270 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1052
ID ACF46820 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1053
ID ACF75677 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1054
ID ADA79983 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1055
ID ACF17337 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054458-A1.
PD 20-MAR-2003.

Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1056
ID ACF23091 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1057
ID ACF08091 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1058
ID ACF08398 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1059
ID ACF40702 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1060
ID ACF53881 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1061
ID ACD47145 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1062
ID ACF48048 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1063
ID ACF47434 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1064
ID ACF46206 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1065
ID ACD86295 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1066
ID ACF52653 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1067
ID ACF52960 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1068
ID ACF64953 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1069
ID ACF76598 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1070
ID ACF61498 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1071
ID ACF61805 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1072
ID ACD30836 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1073
ID ACD31757 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1074
ID ACD32678 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003054477-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1075
ID ACF17644 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1076
ID ACF07477 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1077
ID ACF20635 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1078
ID ACF20942 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1079
ID ACF21249 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1080
ID ACD47759 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1081
ID ACF47741 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1082
ID ACF53574 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1083
ID ACD86909 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1084
ID ACH05157 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1085
ID ACF44654 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1086
ID ADA81710 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1087
ID ACD22309 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1088
ID ACD24656 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1089
ID ACD39859 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1090
ID ACD40166 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1091
ID ACF13474 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1092
ID ACF03276 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1093
ID ACF78747 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.

PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1094
ID ACF11468 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1095
ID ACF50811 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1096
ID ACF34306 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1097
ID ACD46531 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1098
ID ACD48373 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1099
ID ACF27754 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1100
ID ACF24626 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1101
ID ACD85681 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1102
ID ACD90286 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1103
ID ACD83839 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1104
ID ACF49276 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1105
ID ACH07361 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1106
ID ACH07668 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1107
ID ACH08282 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1108
ID ACH11473 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1109
ID ACH11780 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1110
ID ACH10431 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1111
ID ACF01434 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1112

ID ACF41009 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1113
ID ACD24349 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1114
ID ACD31450 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1115
ID ACF17951 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1116
ID ACF32734 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1117
ID ACF40395 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1118
ID ACF48355 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1119
ID ACF38304 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1120
ID ACF25240 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1121
ID ACF27140 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1122
ID ACF29596 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1123
ID ACD87830 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1124
ID ACF76291 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1125
ID ACF49583 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1126
ID ACF44040 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1127
ID ACH06385 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1128
ID ACH06692 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1129
ID ADA83508 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1130
ID ACC92748 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1131

ID ACC93362 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1132
ID ACF19407 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1133
ID ACD13098 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1134
ID ACF06556 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1135
ID ACC94590 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1136
ID ACC98018 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1137
ID ACC94283 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1138
ID ACF42237 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1139
ID ACD31143 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1140
ID ACD43172 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1141
ID ACD43479 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1142
ID ACF15009 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1143
ID ACF01741 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1144
ID ACF31813 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1145
ID ACD67490 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1146
ID ACD48680 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1147
ID ACD48987 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1148
ID ACF51425 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1149
ID ACF54188 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1150
ID ACF25912 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.

PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1151
ID ACF39225 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1152
ID ACF28982 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1153
ID ACD90899 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1154
ID ACD86602 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1155
ID ACH05464 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1156
ID ACF65260 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1157
ID ADB20551 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1158
ID ACF43733 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1159
ID ACH09203 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1160
ID ACH09510 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1161
ID ADA78803 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1162
ID ACF09933 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1163
ID ACF51118 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1164
ID ACF24012 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1165
ID ACD88444 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1166
ID ACH09817 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1167
ID ACH10738 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1168
ID ACD11545 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;

Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1169
ID ACC96595 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1170
ID ACH04380 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1171
ID ACC98625 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1172
ID ACF41930 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1173
ID ACF16851 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1174
ID ACD32371 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1175
ID ACD30529 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1176
ID ACD41400 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1177
ID ACF07784 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1178
ID ACF31199 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1179
ID ACF77519 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1180
ID ACF11161 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1181
ID ACF33041 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1182
ID ACF26219 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1183
ID ACD83532 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1184
ID ACF23705 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1185
ID ACF43119 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1186
ID ACF43426 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1187
ID ACH06078 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;

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  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1188
ID   ACH08896 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1189
ID   ACC90490 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003027273-A1.
PD   06-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1190
ID   ACF10854 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003036119-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1191
ID   ACC93669 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003036120-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1192
ID   ACC96288 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1193
ID   ACD24963 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003044921-A1.
PD   06-MAR-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1194
ID   ACF02048 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1195
ID   ACF22170 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1196
ID   ACF22784 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1197
ID   ACF09012 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1198
ID   ACF33348 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1199
ID   ACF54802 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1200
ID   ACF48662 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1201
ID   ACD47452 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068697-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1202
ID   ACD49294 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1203
ID   ACF37997 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1204
ID   ACF30210 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1205
ID   ACD87523 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1206
ID   ACF62112 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003104538-A1.
PD   05-JUN-2003.
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  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1207
ID   ACH11045 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1208
ID   ACD10210 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003036158-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1209
ID   ACD16935 standard; cDNA; 4277 BP.
DE   cDNA encoding human PRO polypeptide #220.
PN   US2003036151-A1.
PD   20-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1210
ID   ACC99232 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003040067-A1.
PD   27-FEB-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1211
ID   ACF00626 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003054456-A1.
PD   20-MAR-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1212
ID   ACD41093 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1213
ID   ACF14702 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1214
ID   ACF22477 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1215
ID   ACF79054 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1216
ID   ACD67924 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003073129-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1217
ID   ACF11775 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1218
ID   ACF51732 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1219
ID   ACF33655 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1220
ID   ACD49908 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068731-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1221
ID   ACF37690 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003068683-A1.
PD   10-APR-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1222
ID   ACF28675 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003068754-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1223
ID   ACD88751 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003068681-A1.
PD   10-APR-2003.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1224
ID   ACF75370 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003096351-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 9;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1225
ID   ACF61191 standard; cDNA; 4277 BP.
DE   Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN   US2003096358-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1226
ID ACF44347 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1227
ID ACH08589 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1228
ID ACC93976 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1229
ID ACD21081 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1230
ID ACF06863 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1231
ID ACD20774 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1232
ID ACD22923 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1233
ID ACF41623 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1234
ID ACF07170 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1235
ID ACF77826 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1236
ID ACD46224 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1237
ID ACF47127 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1238
ID ACF54495 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1239
ID ACF45899 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1240
ID ACF45592 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1241
ID ACF38611 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1242
ID ACD89672 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1243
ID ACD85374 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1244
ID ACD85988 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003068726-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1245
ID ACF75984 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1246
ID ACF60884 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1247
ID ACH05771 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1248
ID ADA82874 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1249
ID ACF56030 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 3.5%; Score 31; DB 9; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1250
ID ACF55416 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1251
ID ADB86182 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1252
ID ACF56337 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1253
ID ACF56644 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1254
ID ACF55723 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1255
ID ACF55109 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1256
ID ADC17926 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #18.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1257
ID ADD05912 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1258
ID ADD10446 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #79.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1259
ID ADD11406 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #79.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1260
ID ADD70572 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1261
ID ADD39649 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1262
ID ADD70095 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;

RESULT 1263
ID ADD37199 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #79.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1264
ID ADD38216 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1265
ID ADD39172 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1266
ID ADD38695 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1267
ID ADD40126 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1268
ID ADE50347 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1269
ID ADE19959 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1270
ID ADE49870 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1271
ID ADE21428 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1272
ID ADF29853 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1273
ID ADF55746 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1274
ID ADG02907 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1275
ID ADG01614 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1276
ID ADF95789 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1277
ID ADG12604 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1278
ID ADH09264 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1279
ID ADH99250 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1280
ID ABX78747 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1281
ID ACA75719 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003032127-A1.

PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1282
ID ACA71199 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1283
ID ACC87727 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1284
ID ACC87113 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1285
ID ACD04286 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1286
ID ACA69617 standard; cDNA; 4277 BP.
DE cDNA encoding human PRO polypeptide #220.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1287
ID ACA90462 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1288
ID ACC89569 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1289
ID ACA98360 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1290
ID ACA94002 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1291
ID ACD15395 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1292
ID ACD08982 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #220.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1293
ID ACC96902 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1294
ID ACF15623 standard; cDNA; 4277 BP.
DE Human secreted polypeptide PRO1190-encoding cDNA, SEQ ID NO:439.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1295
ID ACA72990 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1296
ID ACD03162 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1297
ID ACD01977 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1298
ID ACA92169 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 31; DB 10; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1299
ID ADL33043 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 11; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1300
ID ADM30579 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 11; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1301
ID ADE41407 standard; cDNA; 4277 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #79.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;

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  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1302
ID   ADE74576 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003211572-A1.
PD   13-NOV-2003.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1303
ID   ADE75188 standard; cDNA; 4277 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #220.
PN   US2003211574-A1.
PD   13-NOV-2003.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1304
ID   ADE96430 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003195347-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1305
ID   ADF25741 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003199675-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1306
ID   ADF24640 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003198993-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1307
ID   ADF29376 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003203401-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1308
ID   ADE96907 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003195334-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1309
ID   ADF96401 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003215909-A1.
PD   20-NOV-2003.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1310
ID   ADG04672 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003215912-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1311
ID   ADG00832 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003215911-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1312
ID   ADG83088 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #220.
PN   US2003215910-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1313
ID   ADH02945 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003216562-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1314
ID   ADH03899 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003220471-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1315
ID   ADH03422 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2003224478-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1316
ID   ADH26369 standard; cDNA; 4277 BP.
DE   Novel human secreted and transmembrane protein PRO1190 cDNA.
PN   US2003068770-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1317
ID   ADH33338 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #220.
PN   US2003068768-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1318
ID   ADH43590 standard; cDNA; 4277 BP.
DE   Human PRO polynucleotide #79.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1319
ID   ADH04376 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2004005626-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 31;  DB 12;  Length 4277;
  Best Local Similarity   52.8%;  Pred. No. 3.3e+02;
RESULT 1320
ID   ADH61377 standard; cDNA; 4277 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1190.
PN   US2004014130-A1.
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PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1321
ID ADJ55077 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1322
ID ADK82935 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #79.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1323
ID ADJ64848 standard; cDNA; 4277 BP.
DE Human PRO polynucleotide #220.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1324
ID ADM31744 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1325
ID ADM36791 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1326
ID ADM40596 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1327
ID ADN05255 standard; cDNA; 4277 BP.
DE Antipsoriatic cDNA sequence #846.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1328
ID ADL94576 standard; cDNA; 4277 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1190.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1329
ID ADN38204 standard; cDNA; 4277 BP.
DE Novel human secreted and transmembrane protein PRO1190 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 31; DB 12; Length 4277;
Best Local Similarity 52.8%; Pred. No. 3.3e+02;
RESULT 1330
ID ADQ22069 standard; DNA; 4605 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4889.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.5%; Score 31; DB 12; Length 4605;
Best Local Similarity 52.8%; Pred. No. 3.5e+02;
RESULT 1331
ID ABL92114 standard; cDNA; 5010 BP.
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 251.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 3.5%; Score 31; DB 6; Length 5010;
Best Local Similarity 56.3%; Pred. No. 3.6e+02;
RESULT 1332
ID ABX72039 standard; DNA; 5010 BP.
DE DNA encoding human tumour endothelial marker TEM 31.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 3.5%; Score 31; DB 10; Length 5010;
Best Local Similarity 56.3%; Pred. No. 3.6e+02;
RESULT 1333
ID ADR24819 standard; DNA; 5010 BP.
DE Breast cancer prognosis marker #680.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 3.5%; Score 31; DB 13; Length 5010;
Best Local Similarity 56.3%; Pred. No. 3.6e+02;
RESULT 1334
ID ADJ56285 standard; cDNA; 5662 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 91.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Query Match 3.5%; Score 31; DB 10; Length 5662;
Best Local Similarity 56.3%; Pred. No. 3.9e+02;
RESULT 1335
ID ADL61863 standard; DNA; 6021 BP.
DE Human ovarian cancer DNA marker #20075.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.5%; Score 31; DB 5; Length 6021;
Best Local Similarity 56.3%; Pred. No. 4e+02;
RESULT 1336
ID ACN89729 standard; DNA; 6021 BP.
DE Breast cancer related marker, seq id 10879.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.5%; Score 31; DB 11; Length 6021;
Best Local Similarity 56.3%; Pred. No. 4e+02;
RESULT 1337
ID AAI58233 standard; cDNA; 6674 BP.
DE Human polynucleotide SEQ ID NO 436.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 31; DB 4; Length 6674;
Best Local Similarity 56.3%; Pred. No. 4.2e+02;
RESULT 1338
ID ADQ98440 standard; cDNA; 6674 BP.

DE DNA encoding human GPCR-like protein seqid 110.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 31; DB 5; Length 6674;
Best Local Similarity 56.3%; Pred. No. 4.2e+02;
RESULT 1339
ID ADB48200 standard; cDNA; 6674 BP.
DE Novel human cDNA SEQ ID NO 110.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 3.5%; Score 31; DB 9; Length 6674;
Best Local Similarity 56.3%; Pred. No. 4.2e+02;
RESULT 1340
ID ADS36475 standard; DNA; 66686 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1689.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.5%; Score 31; DB 13; Length 66686;
Best Local Similarity 51.0%; Pred. No. 1.4e+03;
RESULT 1341
ID ADS36448 standard; DNA; 105314 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1662.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.5%; Score 31; DB 13; Length 105314;
Best Local Similarity 51.0%; Pred. No. 1.8e+03;
RESULT 1342
ID ADP74214 standard; DNA; 144411 BP.
DE Equine herpesvirus 4 genome gM deletion mutant #2.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.5%; Score 31; DB 12; Length 144411;
Best Local Similarity 46.5%; Pred. No. 2.1e+03;
RESULT 1343
ID ADP74215 standard; DNA; 144486 BP.
DE Equine herpesvirus 4 genome gM deletion mutant #3.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.5%; Score 31; DB 12; Length 144486;
Best Local Similarity 46.5%; Pred. No. 2.1e+03;
RESULT 1344
ID ADP74213 standard; DNA; 145444 BP.
DE Equine herpesvirus 4 genome gM deletion mutant #1.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.5%; Score 31; DB 12; Length 145444;
Best Local Similarity 46.5%; Pred. No. 2.2e+03;
RESULT 1345
ID ADP74202 standard; DNA; 145596 BP.
DE Equine herpesvirus 4 genome seqid 2.
PN US2004109873-A1.
PD 10-JUN-2004.
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
Query Match 3.5%; Score 31; DB 12; Length 145596;
Best Local Similarity 46.5%; Pred. No. 2.2e+03;
RESULT 1346
ID ADO25291 standard; cDNA; 191010 BP.
DE Human protein kinase C zeta I/zeta Ii genomic sequence.
PN WO2004041212-A2.
PD 21-MAY-2004.
PA (SACK/) SACKTOR T C.
PA (CRAR/) CRARY J F.
PA (HERN/) HERNANDEZ A I.
PA (MIRR/) MIRRA S.
PA (SHAO/) SHAO C.
Query Match 3.5%; Score 31; DB 12; Length 191010;
Best Local Similarity 57.9%; Pred. No. 2.5e+03;
RESULT 1347
ID ADF79997 standard; DNA; 366 BP.
DE Leukaemia-related DNA sequence #553.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 3.5%; Score 30.8; DB 10; Length 366;
Best Local Similarity 70.7%; Pred. No. 1e+02;
RESULT 1348
ID AAK64571 standard; cDNA; 389 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:9631.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 4; Length 389;
Best Local Similarity 54.4%; Pred. No. 1.1e+02;
RESULT 1349
ID ADA23145 standard; cDNA; 399 BP.
DE Triticum aestivum defensin encoding cDNA SEQ ID NO:337.
PN WO2003000863-A2.
PD 03-JAN-2003.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 30.8; DB 8; Length 399;
Best Local Similarity 48.3%; Pred. No. 1.1e+02;
RESULT 1350
ID AAK62441 standard; cDNA; 449 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:7501.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 4; Length 449;
Best Local Similarity 54.4%; Pred. No. 1.1e+02;
RESULT 1351
ID ABD07782 standard; DNA; 474 BP.
DE Pseudomonas aeruginosa polynucleotide #6386.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 30.8; DB 11; Length 474;
Best Local Similarity 55.7%; Pred. No. 1.2e+02;
RESULT 1352
ID ADB56378 standard; DNA; 574 BP.
DE Toxicity-related gene, SEQ ID 1404.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 30.8; DB 10; Length 574;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 1353
ID ADB50873 standard; DNA; 574 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1415.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 30.8; DB 10; Length 574;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 1354
ID ABT40935 standard; DNA; 574 BP.
DE Toxicity modelling related rat gene SEQ ID No 637.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 30.8; DB 10; Length 574;

Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 1355
ID ADP71985 standard; DNA; 574 BP.
DE Renal toxin progression gene marker #574.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 30.8; DB 12; Length 574;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 1356
ID ADQ21824 standard; DNA; 582 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4644.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.5%; Score 30.8; DB 12; Length 582;
Best Local Similarity 55.7%; Pred. No. 1.3e+02;
RESULT 1357
ID ACA23247 standard; DNA; 825 BP.
DE Prokaryotic essential gene #4904.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.5%; Score 30.8; DB 8; Length 825;
Best Local Similarity 48.8%; Pred. No. 1.6e+02;
RESULT 1358
ID ADF50940 standard; cDNA; 831 BP.
DE Human HN1 cDNA clone (SeqID 39).
PN WO2003060164-A1.
PD 24-JUL-2003.
PA (ARCT-) ARCTURUS ENG INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.5%; Score 30.8; DB 10; Length 831;
Best Local Similarity 49.7%; Pred. No. 1.6e+02;
RESULT 1359
ID ADD34429 standard; DNA; 852 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:2207.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match 3.5%; Score 30.8; DB 10; Length 852;
Best Local Similarity 55.1%; Pred. No. 1.6e+02;
RESULT 1360
ID ADR26085 standard; DNA; 874 BP.
DE Breast cancer prognosis marker #1946.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 3.5%; Score 30.8; DB 13; Length 874;
Best Local Similarity 70.7%; Pred. No. 1.6e+02;
RESULT 1361
ID AAD42241 standard; cDNA; 893 BP.
DE Corn FT homologue cDNA #2.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 30.8; DB 6; Length 893;
Best Local Similarity 47.7%; Pred. No. 1.7e+02;
RESULT 1362
ID ADR04246 standard; cDNA; 893 BP.
DE Corn FT homologue encoding cDNA SEQ ID NO:13.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.5%; Score 30.8; DB 13; Length 893;
Best Local Similarity 47.7%; Pred. No. 1.7e+02;
RESULT 1363
ID ABD07519 standard; DNA; 900 BP.
DE Pseudomonas aeruginosa polynucleotide #6123.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 30.8; DB 11; Length 900;
Best Local Similarity 47.4%; Pred. No. 1.7e+02;
RESULT 1364
ID ACA35267 standard; DNA; 975 BP.
DE Prokaryotic essential gene #16924.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.5%; Score 30.8; DB 8; Length 975;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
RESULT 1365
ID ADO29045 standard; cDNA; 1071 BP.
DE Mouse novel GPCR GPR20 polynucleotide, SEQ ID NO:144.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 3.5%; Score 30.8; DB 12; Length 1071;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
RESULT 1366
ID ABD07557 standard; DNA; 1173 BP.
DE Pseudomonas aeruginosa polynucleotide #6161.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 30.8; DB 11; Length 1173;
Best Local Similarity 55.7%; Pred. No. 1.9e+02;
RESULT 1367
ID AAS51572 standard; DNA; 1365 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #157.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.5%; Score 30.8; DB 4; Length 1365;
Best Local Similarity 55.7%; Pred. No. 2.1e+02;
RESULT 1368
ID ACA19425 standard; DNA; 1365 BP.
DE Prokaryotic essential gene #1082.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.5%; Score 30.8; DB 8; Length 1365;
Best Local Similarity 55.7%; Pred. No. 2.1e+02;
RESULT 1369
ID ABD07400 standard; DNA; 1494 BP.
DE Pseudomonas aeruginosa polynucleotide #6004.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 30.8; DB 11; Length 1494;
Best Local Similarity 55.7%; Pred. No. 2.2e+02;
RESULT 1370
ID AAC60999 standard; cDNA; 1535 BP.
DE Human vesicle associated protein 15 encoding cDNA SEQ ID NO:34.
PN WO200060082-A2.
PD 12-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 3.5%; Score 30.8; DB 3; Length 1535;
Best Local Similarity 49.4%; Pred. No. 2.2e+02;
RESULT 1371
ID ABL26578 standard; DNA; 2507 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31207.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 30.8; DB 4; Length 2507;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
RESULT 1372
ID ADQ22847 standard; DNA; 3491 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5667.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 3.5%; Score 30.8; DB 12; Length 3491;
Best Local Similarity 70.7%; Pred. No. 3.4e+02;
RESULT 1373
ID AAH57554 standard; cDNA; 4615 BP.
DE Human brain cell specific cDNA sequence SEQ ID NO:394.
PN WO200132927-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.5%; Score 30.8; DB 4; Length 4615;
Best Local Similarity 70.7%; Pred. No. 4e+02;
RESULT 1374
ID ADF81694 standard; DNA; 4701 BP.
DE Leukaemia-related DNA sequence #2250.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 3.5%; Score 30.8; DB 10; Length 4701;
Best Local Similarity 70.7%; Pred. No. 4e+02;
RESULT 1375
ID ADF81692 standard; DNA; 4701 BP.
DE Leukaemia-related DNA sequence #2248.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 3.5%; Score 30.8; DB 10; Length 4701;
Best Local Similarity 70.7%; Pred. No. 4e+02;
RESULT 1376
ID ADF81693 standard; DNA; 4701 BP.
DE Leukaemia-related DNA sequence #2249.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 3.5%; Score 30.8; DB 10; Length 4701;
Best Local Similarity 70.7%; Pred. No. 4e+02;
RESULT 1377
ID ADI61748 standard; cDNA; 4852 BP.
DE Human cDNA upregulated in Alzheimer's disease, INCYTE 197687.11.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.5%; Score 30.8; DB 12; Length 4852;
Best Local Similarity 70.7%; Pred. No. 4.1e+02;
RESULT 1378
ID ADN04391 standard; cDNA; 4860 BP.
DE Antipsoriatic cDNA sequence #396.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 30.8; DB 12; Length 4860;
Best Local Similarity 70.7%; Pred. No. 4.1e+02;
RESULT 1379
ID AAC55840 standard; DNA; 12249 BP.
DE Complete Mitomycin ORF 1-9 nucleotide sequence.
PN WO200053737-A2.
PD 14-SEP-2000.
PA (MINU) UNIV MINNESOTA.
PA (SHER/) SHERMAN D H.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELDON P C.
Query Match 3.5%; Score 30.8; DB 3; Length 12249;
Best Local Similarity 61.0%; Pred. No. 6.8e+02;
RESULT 1380
ID ADE10259 standard; DNA; 12249 BP.
DE S. lavendulae mitomycin C gene cluster for ORFs 1-9.
PN US2003134398-A1.
PD 17-JUL-2003.
PA (SHER/) SHERMAN D H.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELDON P.
Query Match 3.5%; Score 30.8; DB 10; Length 12249;
Best Local Similarity 61.0%; Pred. No. 6.8e+02;
RESULT 1381
ID AAS35116 standard; DNA; 13795 BP.
DE DNA #66 encoding human neoplastic disease associated polypeptide.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 4; Length 13795;
Best Local Similarity 53.3%; Pred. No. 7.2e+02;
RESULT 1382
ID AAS31474 standard; DNA; 13795 BP.
DE Human DNA for a novel extracellular matrix protein, Seq ID No 553.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 4; Length 13795;
Best Local Similarity 53.3%; Pred. No. 7.2e+02;
RESULT 1383
ID ABA06834 standard; DNA; 13795 BP.
DE Human genomic DNA SEQ ID NO: 920.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 4; Length 13795;
Best Local Similarity 53.3%; Pred. No. 7.2e+02;
RESULT 1384
ID ABQ66798 standard; DNA; 13795 BP.
DE Human polynucleotide SEQ ID NO 553.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.5%; Score 30.8; DB 6; Length 13795;
Best Local Similarity 53.3%; Pred. No. 7.2e+02;
RESULT 1385
ID ABV84171 standard; DNA; 13795 BP.
DE Human polynucleotide SEQ ID NO 920.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.5%; Score 30.8; DB 6; Length 13795;
Best Local Similarity 53.3%; Pred. No. 7.2e+02;
RESULT 1386
ID ADC11085 standard; DNA; 13795 BP.
DE Human DNA from extracelluar matrix gene 47 #2.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 10; Length 13795;
Best Local Similarity 53.3%; Pred. No. 7.2e+02;
RESULT 1387
ID ADC46558 standard; DNA; 13795 BP.
DE Human neoplastic disease-associated gene 116 DNA #2.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 10; Length 13795;

Best Local Similarity 53.3%; Pred. No. 7.2e+02;
RESULT 1388
ID AAK80090 standard; DNA; 15177 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34902.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 4; Length 15177;
Best Local Similarity 70.7%; Pred. No. 7.6e+02;
RESULT 1389
ID AAK66169 standard; DNA; 15177 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20981.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 30.8; DB 4; Length 15177;
Best Local Similarity 70.7%; Pred. No. 7.6e+02;
RESULT 1390
ID AAC55857 standard; DNA; 18331 BP.
DE Complete nucleotide sequence of the mitomycin gene cluster.
PN WO200053737-A2.
PD 14-SEP-2000.
PA (MINU) UNIV MINNESOTA.
PA (SHER/) SHERMAN D H.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELDON P C.
Query Match 3.5%; Score 30.8; DB 3; Length 18331;
Best Local Similarity 61.0%; Pred. No. 8.4e+02;
RESULT 1391
ID ADE10266 standard; DNA; 18331 BP.
DE S. lavendulae mitomycin gene cluster complete sequence.
PN US2003134398-A1.
PD 17-JUL-2003.
PA (SHER/) SHERMAN D H.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELDON P.
Query Match 3.5%; Score 30.8; DB 10; Length 18331;
Best Local Similarity 61.0%; Pred. No. 8.4e+02;
RESULT 1392
ID ADC86184 standard; DNA; 43818 BP.
DE Human GPCR gene SEQ ID NO:637.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.5%; Score 30.8; DB 10; Length 43818;
Best Local Similarity 47.8%; Pred. No. 1.3e+03;
RESULT 1393
ID ACN43926 standard; DNA; 53242 BP.
DE Human genomic sequence hCG1782215.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 30.8; DB 11; Length 53242;
Best Local Similarity 51.4%; Pred. No. 1.5e+03;
RESULT 1394
ID ACN43986 standard; DNA; 73995 BP.
DE Human genomic sequence hCG40211.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 30.8; DB 11; Length 73995;
Best Local Similarity 55.7%; Pred. No. 1.8e+03;
RESULT 1395
ID ADQ97980 standard; DNA; 97081 BP.
DE Human cancer associated sequence HD11-034, SEQ ID 957.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 30.8; DB 12; Length 97081;
Best Local Similarity 51.4%; Pred. No. 2e+03;
RESULT 1396
Query Match 3.5%; Score 30.8; DB 11; Length 110000;
Best Local Similarity 55.7%; Pred. No. 2.2e+03;
RESULT 1397
Query Match 3.5%; Score 30.8; DB 12; Length 110000;
Best Local Similarity 55.7%; Pred. No. 2.2e+03;
RESULT 1398
ID ABD32827 standard; DNA; 129381 BP.
DE Human cancer-associated genomic DNA HD17-008.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 30.8; DB 13; Length 129381;
Best Local Similarity 47.8%; Pred. No. 2.3e+03;
RESULT 1399
ID ADF57870 standard; cDNA; 186 BP.
DE Human polynucleotide sequence SEQ ID NO:237.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.4%; Score 30.6; DB 10; Length 186;
Best Local Similarity 58.1%; Pred. No. 83;
RESULT 1400
ID AAL00525 standard; cDNA; 360 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 526.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.6; DB 4; Length 360;
Best Local Similarity 55.0%; Pred. No. 1.2e+02;
RESULT 1401
ID ABQ54812 standard; cDNA; 360 BP.
DE Human ovarian antigen HOFMK22 cDNA, SEQ ID NO:692.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.6; DB 6; Length 360;
Best Local Similarity 55.0%; Pred. No. 1.2e+02;
RESULT 1402
ID AAH12307 standard; cDNA; 490 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:9142.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.4%; Score 30.6; DB 4; Length 490;
Best Local Similarity 48.6%; Pred. No. 1.4e+02;
RESULT 1403
ID ACH13407 standard; cDNA; 496 BP.
DE Human adult brain cDNA #619.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.4%; Score 30.6; DB 9; Length 496;
Best Local Similarity 54.8%; Pred. No. 1.4e+02;
RESULT 1404
ID AAC55789 standard; DNA; 531 BP.
DE Mitomycin gene cluster related DNA sequence SEQ ID 23.
PN WO200053737-A2.
PD 14-SEP-2000.
PA (MINU) UNIV MINNESOTA.
PA (SHER/) SHERMAN D H.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELDON P C.
Query Match 3.4%; Score 30.6; DB 3; Length 531;
Best Local Similarity 62.3%; Pred. No. 1.4e+02;

RESULT 1405
ID ADE10208 standard; DNA; 531 BP.
DE S. lavendulae mitomycin biosynthsis associated DNA #2.
PN US2003134398-A1.
PD 17-JUL-2003.
PA (SHER/) SHERMAN D H.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELDON P.
Query Match 3.4%; Score 30.6; DB 10; Length 531;
Best Local Similarity 62.3%; Pred. No. 1.4e+02;
RESULT 1406
ID ABZ13163 standard; DNA; 534 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 968.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.4%; Score 30.6; DB 6; Length 534;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
RESULT 1407
ID AAK92581 standard; cDNA; 550 BP.
DE Human cDNA 3'-end sequence, SEQ ID NO: 1041.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.4%; Score 30.6; DB 4; Length 550;
Best Local Similarity 65.2%; Pred. No. 1.5e+02;
RESULT 1408
ID ADL29008 standard; cDNA; 550 BP.
DE 3' end of a human cDNA molecule SeqID 1041.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.4%; Score 30.6; DB 12; Length 550;
Best Local Similarity 65.2%; Pred. No. 1.5e+02;
RESULT 1409
ID ABQ47222 standard; DNA; 558 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33813.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 30.6; DB 6; Length 558;
Best Local Similarity 48.6%; Pred. No. 1.5e+02;
RESULT 1410
ID ABQ47223 standard; DNA; 558 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33814.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 30.6; DB 6; Length 558;
Best Local Similarity 48.6%; Pred. No. 1.5e+02;
RESULT 1411
ID ACF04310 standard; DNA; 604 BP.
DE M parafortuitum hsp65 gene fragment.
PN WO2003062470-A1.
PD 31-JUL-2003.
PA (BIOM-) BIOMEDLAB CORP.
PA (KIMB/) KIM B.
Query Match 3.4%; Score 30.6; DB 9; Length 604;
Best Local Similarity 48.6%; Pred. No. 1.6e+02;
RESULT 1412
ID ADI43365 standard; DNA; 613 BP.
DE Plant transcription factor polynucleotide #1247.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 3.4%; Score 30.6; DB 12; Length 613;
Best Local Similarity 49.1%; Pred. No. 1.6e+02;
RESULT 1413
ID ABQ65526 standard; DNA; 731 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 103.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 3.4%; Score 30.6; DB 6; Length 731;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
RESULT 1414
ID AAC47107 standard; DNA; 787 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52590.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 3.4%; Score 30.6; DB 3; Length 787;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
RESULT 1415
ID AAV66761 standard; DNA; 824 BP.
DE Pathogen response protein LSD1-interacting protein II DNA.
PN WO9837755-A1.
PD 03-SEP-1998.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match 3.4%; Score 30.6; DB 2; Length 824;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
RESULT 1416
ID ABK68665 standard; DNA; 939 BP.
DE Human DNA for olfactory and pheromone G protein-coupled receptor #265.
PN WO200224726-A2.
PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.
Query Match 3.4%; Score 30.6; DB 6; Length 939;
Best Local Similarity 53.8%; Pred. No. 2e+02;
RESULT 1417
ID ADG83525 standard; DNA; 939 BP.
DE Human Olfactory and pheromone GPCR DNA #120.
PN US2003221205-A1.
PD 27-NOV-2003.
PA (VEIT/) VEITHEN A.
Query Match 3.4%; Score 30.6; DB 12; Length 939;
Best Local Similarity 53.8%; Pred. No. 2e+02;
RESULT 1418
ID ABS64716 standard; cDNA; 999 BP.
DE cDNA encoding human GPCR9 protein.
PN WO200264793-A2.
PD 22-AUG-2002.

PA (CURA-) CURAGEN CORP.
Query Match 3.4%; Score 30.6; DB 6; Length 999;
Best Local Similarity 53.8%; Pred. No. 2e+02;
RESULT 1419
ID ABL63119 standard; DNA; 1098 BP.
DE Breast cancer related gene sequence SEQ ID NO:1456.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.4%; Score 30.6; DB 6; Length 1098;
Best Local Similarity 51.1%; Pred. No. 2.1e+02;
RESULT 1420
ID ADA06078 standard; DNA; 1098 BP.
DE Mouse NOV55c gene sequence SEQ ID NO:438.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.4%; Score 30.6; DB 8; Length 1098;
Best Local Similarity 49.7%; Pred. No. 2.1e+02;
RESULT 1421
ID ADJ74823 standard; DNA; 1098 BP.
DE Marker gene SEQ ID NO:75.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 3.4%; Score 30.6; DB 12; Length 1098;
Best Local Similarity 51.1%; Pred. No. 2.1e+02;
RESULT 1422
ID ADL83256 standard; cDNA; 1098 BP.
DE Human DNA269599, SEQ ID 458.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.4%; Score 30.6; DB 12; Length 1098;
Best Local Similarity 51.1%; Pred. No. 2.1e+02;
RESULT 1423
ID ADQ17497 standard; DNA; 1098 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 314.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.4%; Score 30.6; DB 12; Length 1098;
Best Local Similarity 51.1%; Pred. No. 2.1e+02;
RESULT 1424
ID ADR52825 standard; DNA; 1098 BP.
DE Drug therapy altered expressed gene #176.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 3.4%; Score 30.6; DB 13; Length 1098;
Best Local Similarity 51.1%; Pred. No. 2.1e+02;
RESULT 1425
ID ACC49337 standard; cDNA; 1100 BP.
DE Human G protein-coupled receptor GCREC-11 encoding cDNA SEQ ID NO:33.
PN WO2003023009-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.4%; Score 30.6; DB 8; Length 1100;
Best Local Similarity 53.8%; Pred. No. 2.1e+02;
RESULT 1426
ID ADD19003 standard; DNA; 1190 BP.
DE Human disease related protein DNA sequence SeqID492.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 3.4%; Score 30.6; DB 10; Length 1190;
Best Local Similarity 51.1%; Pred. No. 2.2e+02;
RESULT 1427
ID ADL83123 standard; cDNA; 1190 BP.
DE Human PRO84707 cDNA, SEQ ID 325.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.4%; Score 30.6; DB 12; Length 1190;
Best Local Similarity 51.1%; Pred. No. 2.2e+02;
RESULT 1428
ID ADR14234 standard; DNA; 1190 BP.
DE Human NF-kappaB pathway-associated gene SeqID235.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.4%; Score 30.6; DB 13; Length 1190;
Best Local Similarity 51.1%; Pred. No. 2.2e+02;
RESULT 1429
ID ABX63538 standard; cDNA; 1218 BP.
DE Human cDNA #538 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 3.4%; Score 30.6; DB 8; Length 1218;
Best Local Similarity 51.1%; Pred. No. 2.3e+02;
RESULT 1430
ID AAK53362 standard; cDNA; 1230 BP.
DE Human polynucleotide SEQ ID NO 2891.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.4%; Score 30.6; DB 4; Length 1230;
Best Local Similarity 51.1%; Pred. No. 2.3e+02;
RESULT 1431
ID ADQ22208 standard; DNA; 1309 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5028.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.4%; Score 30.6; DB 12; Length 1309;
Best Local Similarity 51.1%; Pred. No. 2.4e+02;
RESULT 1432
ID ADC85970 standard; DNA; 1339 BP.
DE Human GPCR gene SEQ ID NO:423.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.4%; Score 30.6; DB 10; Length 1339;
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
RESULT 1433
ID AAS33246 standard; cDNA; 1446 BP.
DE DNA encoding human secreted protein, Seq ID No 205.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.6; DB 4; Length 1446;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
RESULT 1434
ID ADJ75889 standard; DNA; 1560 BP.
DE Marker gene SEQ ID NO:1141.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 3.4%; Score 30.6; DB 12; Length 1560;
Best Local Similarity 49.7%; Pred. No. 2.6e+02;
RESULT 1435
ID ADJ75858 standard; DNA; 1560 BP.
DE Marker gene SEQ ID NO:1110.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 3.4%; Score 30.6; DB 12; Length 1560;
Best Local Similarity 49.7%; Pred. No. 2.6e+02;
RESULT 1436
ID AAQ01765 standard; cDNA; 1665 BP.

DE Sequence of perforin cDNA.
PN JP02002350-A.
PD 08-JAN-1990.
PA (SUME) SUMITOMO ELECTRIC IND CO.
Query Match 3.4%; Score 30.6; DB 2; Length 1665;
Best Local Similarity 50.3%; Pred. No. 2.7e+02;
RESULT 1437
ID ADQ63394 standard; cDNA; 1732 BP.
DE Novel human cDNA sequence #555.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.4%; Score 30.6; DB 12; Length 1732;
Best Local Similarity 48.6%; Pred. No. 2.7e+02;
RESULT 1438
ID AAK69401 standard; DNA; 2633 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24213.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.6; DB 4; Length 2633;
Best Local Similarity 56.4%; Pred. No. 3.4e+02;
RESULT 1439
ID AAI63869 standard; cDNA; 2649 BP.
DE Human polynucleotide SEQ ID NO 77.
PN WO200155308-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.6; DB 4; Length 2649;
Best Local Similarity 52.0%; Pred. No. 3.4e+02;
RESULT 1440
ID ADM24420 standard; cDNA; 2649 BP.
DE Human PRO polynucleotide #67.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.6; DB 12; Length 2649;
Best Local Similarity 52.0%; Pred. No. 3.4e+02;
RESULT 1441
ID ADR07046 standard; cDNA; 2670 BP.
DE Full length human cDNA useful for treating neurological disease Seq 552.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.4%; Score 30.6; DB 13; Length 2670;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
RESULT 1442
ID ABZ77849 standard; cDNA; 3096 BP.
DE Human fusion protein-19.8 coding sequence.
PN CN1376680-A.
PD 30-OCT-2002.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 3.4%; Score 30.6; DB 8; Length 3096;
Best Local Similarity 48.6%; Pred. No. 3.7e+02;
RESULT 1443
ID ACC46115 standard; cDNA; 3327 BP.
DE Human dithp enzyme-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.4%; Score 30.6; DB 8; Length 3327;
Best Local Similarity 56.4%; Pred. No. 3.9e+02;
RESULT 1444
ID ADQ22784 standard; DNA; 4097 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5604.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.4%; Score 30.6; DB 12; Length 4097;
Best Local Similarity 51.9%; Pred. No. 4.3e+02;
RESULT 1445
ID AAF88336 standard; DNA; 6459 BP.
DE S. spinosa DNA fragment encoding ORF19, SEQ ID 43.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Query Match 3.4%; Score 30.6; DB 4; Length 6459;
Best Local Similarity 68.9%; Pred. No. 5.5e+02;
RESULT 1446
ID AAA10594 standard; DNA; 10732 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 3.4%; Score 30.6; DB 3; Length 10732;
Best Local Similarity 20.2%; Pred. No. 7.3e+02;
RESULT 1447
ID AAS12439 standard; DNA; 37590 BP.
DE DNA encoding 1-aminocyclopropane carboxylate synthase #10.
PN WO200168879-A2.
PD 20-SEP-2001.
PA (FARB) BAYER AG.
Query Match 3.4%; Score 30.6; DB 4; Length 37590;
Best Local Similarity 56.4%; Pred. No. 1.4e+03;
RESULT 1448
ID ACN44904 standard; DNA; 40463 BP.
DE Mouse genomic sequence mCG5448.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.4%; Score 30.6; DB 11; Length 40463;
Best Local Similarity 56.4%; Pred. No. 1.5e+03;
RESULT 1449
ID ABD33576 standard; DNA; 45315 BP.
DE Murine cancer-associated (CA) gene MD07-116.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 30.6; DB 13; Length 45315;
Best Local Similarity 50.3%; Pred. No. 1.6e+03;
RESULT 1450
ID AAF88313 standard; DNA; 50000 BP.
DE S. spinosa DNA fragment SEQ ID 2.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Query Match 3.4%; Score 30.6; DB 4; Length 50000;
Best Local Similarity 68.9%; Pred. No. 1.6e+03;
RESULT 1451
ID AAF88316 standard; DNA; 50000 BP.
DE S. spinosa DNA fragment SEQ ID 5.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Query Match 3.4%; Score 30.6; DB 4; Length 50000;
Best Local Similarity 68.9%; Pred. No. 1.6e+03;
RESULT 1452
ID ABV75557 standard; DNA; 75236 BP.
DE Saccharopolyspora butenyl-spinosyn biosynthetic gene cluster 1.
PN WO200279477-A2.
PD 10-OCT-2002.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.4%; Score 30.6; DB 10; Length 75236;
Best Local Similarity 68.9%; Pred. No. 2e+03;
RESULT 1453
ID AAZ21501 standard; DNA; 80161 BP.
DE DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes.
Query Match 3.4%; Score 30.6; DB 2; Length 80161;
Best Local Similarity 68.9%; Pred. No. 2.1e+03;
RESULT 1454
ID AAF22303 standard; DNA; 611590 BP.
DE Arabidopsis thaliana chromosome 2 centromere.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.

Query Match 3.4%; Score 30.6; DB 3; Length 110000;
Best Local Similarity 53.8%; Pred. No. 2.5e+03;
RESULT 1455
ID ADH50806 standard; DNA; 119596 BP.
DE Human G-protein coupled receptor gene.
Query Match 3.4%; Score 30.6; DB 6; Length 119596;
Best Local Similarity 51.9%; Pred. No. 2.6e+03;
RESULT 1456
ID ADQ97167 standard; DNA; 176771 BP.
DE Human cancer associated sequence HD2-08-009, SEQ ID 143.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 30.6; DB 12; Length 176771;
Best Local Similarity 52.8%; Pred. No. 3.1e+03;
RESULT 1457
ID ABL76543 standard; cDNA; 293 BP.
DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5917.
PN US2001051335-A1.
PD 13-DEC-2001.
PA (LALG/) LALGUDI R V.
PA (ITOL/) ITO L Y.
PA (SHER/) SHERMAN B K.
Query Match 3.4%; Score 30.4; DB 6; Length 293;
Best Local Similarity 48.7%; Pred. No. 1.2e+02;
RESULT 1458
ID AAD50776 standard; DNA; 526 BP.
DE Clone-B1 DNA used to illustrate the method of the invention.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.4%; Score 30.4; DB 8; Length 526;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1459
ID AAD50777 standard; DNA; 532 BP.
DE Clone-B5 DNA used to illustrate the method of the invention.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.4%; Score 30.4; DB 8; Length 532;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1460
ID AAD50779 standard; DNA; 533 BP.
DE Clone-B10 DNA used to illustrate the method of the invention.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.4%; Score 30.4; DB 8; Length 533;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1461
ID AAD50770 standard; DNA; 534 BP.
DE Clone-B63 DNA used to illustrate the method of the invention.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.4%; Score 30.4; DB 8; Length 534;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1462
ID AAD50769 standard; DNA; 534 BP.
DE Clone-B62 DNA used to illustrate the method of the invention.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.4%; Score 30.4; DB 8; Length 534;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1463
ID AAD50771 standard; DNA; 534 BP.
DE Clone-B67 DNA used to illustrate the method of the invention.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.4%; Score 30.4; DB 8; Length 534;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1464
ID AAD50765 standard; DNA; 579 BP.
DE Pantoea agglomerans chitinase gene.
PN WO200295024-A1.
PD 28-NOV-2002.
PA (MICR-) MICROID CO LTD.
PA (HONG/) HONG S G.
Query Match 3.4%; Score 30.4; DB 8; Length 579;
Best Local Similarity 49.4%; Pred. No. 1.8e+02;
RESULT 1465
ID ADP75767 standard; DNA; 579 BP.
DE DNA sequence relating to the invention SEQ ID NO:4.
PN KR2003060271-A.
PD 16-JUL-2003.
PA (HONG/) HONG S G.
PA (MICR-) MICROID CO LTD.
Query Match 3.4%; Score 30.4; DB 12; Length 579;
Best Local Similarity 49.4%; Pred. No. 1.8e+02;
RESULT 1466
ID ACF04308 standard; DNA; 604 BP.
DE M vaccae hsp65 gene fragment.
PN WO2003062470-A1.
PD 31-JUL-2003.
PA (BIOM-) BIOMEDLAB CORP.
PA (KIMB/) KIM B.
Query Match 3.4%; Score 30.4; DB 9; Length 604;
Best Local Similarity 48.8%; Pred. No. 1.8e+02;
RESULT 1467
ID AAD42236 standard; cDNA; 615 BP.
DE Balsam pear FT homologue cDNA.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.4%; Score 30.4; DB 6; Length 615;
Best Local Similarity 57.3%; Pred. No. 1.8e+02;
RESULT 1468
ID ADR04236 standard; cDNA; 615 BP.
DE Balsam pear FT homologue encoding cDNA SEQ ID NO:3.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.4%; Score 30.4; DB 13; Length 615;
Best Local Similarity 57.3%; Pred. No. 1.8e+02;
RESULT 1469
ID AAS94340 standard; cDNA; 701 BP.
DE DNA encoding novel human diagnostic protein #30144.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.4%; Score 30.4; DB 5; Length 701;
Best Local Similarity 57.3%; Pred. No. 1.9e+02;
RESULT 1470
ID ABK36121 standard; cDNA; 836 BP.
DE cDNA sequence #512 encoding novel human secreted protein.
PN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 3.4%; Score 30.4; DB 6; Length 836;
Best Local Similarity 50.7%; Pred. No. 2.1e+02;
RESULT 1471
ID AAD42237 standard; cDNA; 859 BP.
DE Garden balsam FT homologue cDNA from clone ids.pk0031.a5.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 3.4%; Score 30.4; DB 6; Length 859;

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  Best Local Similarity   57.3%;  Pred. No. 2.2e+02;
RESULT 1472
ID   ADR04238 standard; cDNA; 859 BP.
DE   Garden balsam FT homologue encoding cDNA SEQ ID NO:5.
PN   WO2004067723-A2.
PD   12-AUG-2004.
PA   (PION-) PIONEER HI-BRED INT INC.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
  Query Match             3.4%;  Score 30.4;  DB 13;  Length 859;
  Best Local Similarity   57.3%;  Pred. No. 2.2e+02;
RESULT 1473
ID   AAD42253 standard; cDNA; 969 BP.
DE   Soybean FT homologue cDNA from clone srr2c.pk002.o7.
PN   WO200244390-A2.
PD   06-JUN-2002.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
  Query Match             3.4%;  Score 30.4;  DB 6;  Length 969;
  Best Local Similarity   51.5%;  Pred. No. 2.3e+02;
RESULT 1474
ID   ADR04270 standard; cDNA; 969 BP.
DE   Soybean FT homologue encoding cDNA SEQ ID NO:37.
PN   WO2004067723-A2.
PD   12-AUG-2004.
PA   (PION-) PIONEER HI-BRED INT INC.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
  Query Match             3.4%;  Score 30.4;  DB 13;  Length 969;
  Best Local Similarity   51.5%;  Pred. No. 2.3e+02;
RESULT 1475
ID   ADB12396 standard; DNA; 1002 BP.
DE   Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:6319.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
  Query Match             3.4%;  Score 30.4;  DB 9;  Length 1002;
  Best Local Similarity   59.1%;  Pred. No. 2.4e+02;
RESULT 1476
ID   ADB12398 standard; DNA; 1002 BP.
DE   Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:6317.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
  Query Match             3.4%;  Score 30.4;  DB 9;  Length 1002;
  Best Local Similarity   59.1%;  Pred. No. 2.4e+02;
RESULT 1477
ID   ADB12394 standard; DNA; 1002 BP.
DE   Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:6321.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
  Query Match             3.4%;  Score 30.4;  DB 9;  Length 1002;
  Best Local Similarity   59.1%;  Pred. No. 2.4e+02;
RESULT 1478
ID   AAZ65297 standard; DNA; 1267 BP.
DE   Human secreted protein gene 48.
PN   WO9958660-A1.
PD   18-NOV-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 30.4;  DB 3;  Length 1267;
  Best Local Similarity   50.7%;  Pred. No. 2.7e+02;
RESULT 1479
ID   AAC99825 standard; cDNA; 1267 BP.
DE   Human secreted protein gene 8 SEQ ID NO:18.
PN   WO200070042-A1.
PD   23-NOV-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 30.4;  DB 3;  Length 1267;
  Best Local Similarity   50.7%;  Pred. No. 2.7e+02;
RESULT 1480
ID   ADE11686 standard; cDNA; 1267 BP.
DE   Human secreted polypeptide cDNA #48.
PN   US2003100051-A1.
PD   29-MAY-2003.
PA   (RUBE/) RUBEN S M.
PA   (FLOR/) FLORENCE K A.
PA   (NIJJ/) NI J.
PA   (ROSE/) ROSEN C A.
PA   (CART/) CARTER K C.
PA   (MOOR/) MOORE P A.
PA   (OLSE/) OLSEN H S.
PA   (SHIY/) SHI Y.
PA   (YOUN/) YOUNG P E.
PA   (WEIY/) WEI Y.
PA   (BREW/) BREWER L A.
PA   (SOPP/) SOPPET D R.
PA   (LAFL/) LAFLEUR D W.
PA   (ENDR/) ENDRESS G A.
PA   (EBNE/) EBNER R.
PA   (BIRS/) BIRSE C E.
  Query Match             3.4%;  Score 30.4;  DB 10;  Length 1267;
  Best Local Similarity   50.7%;  Pred. No. 2.7e+02;
RESULT 1481
ID   ADN43083 standard; cDNA; 1316 BP.
DE   Human secreted protein SECP-69 cDNA.
PN   WO2004037987-A2.
PD   06-MAY-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.4%;  Score 30.4;  DB 12;  Length 1316;
  Best Local Similarity   55.8%;  Pred. No. 2.7e+02;
RESULT 1482
ID   ACA37713 standard; DNA; 1422 BP.
DE   Prokaryotic essential gene #19370.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match             3.4%;  Score 30.4;  DB 8;  Length 1422;
  Best Local Similarity   59.1%;  Pred. No. 2.8e+02;
RESULT 1483
ID   ADD71171 standard; cDNA; 1497 BP.
DE   Human intracellular signalling molecule INTSIG-8 cDNA SEQ ID NO:60.
PN   WO2003039348-A2.
PD   15-MAY-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.4%;  Score 30.4;  DB 10;  Length 1497;
  Best Local Similarity   50.7%;  Pred. No. 2.9e+02;
RESULT 1484
ID   AAK94087 standard; cDNA; 1772 BP.
DE   Human full-length cDNA, SEQ ID NO: 2547.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
  Query Match             3.4%;  Score 30.4;  DB 4;  Length 1772;
  Best Local Similarity   50.7%;  Pred. No. 3.2e+02;
RESULT 1485
ID   ADL30514 standard; cDNA; 1772 BP.
DE   Full length human cDNA clone SeqID 2547.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             3.4%;  Score 30.4;  DB 12;  Length 1772;
  Best Local Similarity   50.7%;  Pred. No. 3.2e+02;
RESULT 1486
ID   ACN43749 standard; cDNA; 1882 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2624.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.4%;  Score 30.4;  DB 13;  Length 1882;
  Best Local Similarity   55.8%;  Pred. No. 3.3e+02;
RESULT 1487
ID   ACN43748 standard; cDNA; 1888 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2623.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.4%;  Score 30.4;  DB 13;  Length 1888;
  Best Local Similarity   55.8%;  Pred. No. 3.3e+02;
```

RESULT 1488
ID AAK94805 standard; cDNA; 1962 BP.
DE Human full-length cDNA, SEQ ID NO: 3932.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.4%; Score 30.4; DB 4; Length 1962;
Best Local Similarity 50.7%; Pred. No. 3.4e+02;
RESULT 1489
ID ADL31899 standard; cDNA; 1962 BP.
DE Full length human cDNA clone SeqID 3932.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.4%; Score 30.4; DB 12; Length 1962;
Best Local Similarity 50.7%; Pred. No. 3.4e+02;
RESULT 1490
ID ADQ83908 standard; cDNA; 1968 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #722.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.4%; Score 30.4; DB 12; Length 1968;
Best Local Similarity 50.7%; Pred. No. 3.4e+02;
RESULT 1491
ID ADQ86321 standard; cDNA; 1968 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3193.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.4%; Score 30.4; DB 12; Length 1968;
Best Local Similarity 50.7%; Pred. No. 3.4e+02;
RESULT 1492
ID ADQ83227 standard; cDNA; 1968 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #41.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.4%; Score 30.4; DB 13; Length 1968;
Best Local Similarity 50.7%; Pred. No. 3.4e+02;
RESULT 1493
ID ADQ85136 standard; cDNA; 1968 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1950.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.4%; Score 30.4; DB 13; Length 1968;
Best Local Similarity 50.7%; Pred. No. 3.4e+02;
RESULT 1494
ID ADB63671 standard; cDNA; 2420 BP.
DE Human cDNA encoding clone THYMU20145990.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.4%; Score 30.4; DB 10; Length 2420;
Best Local Similarity 50.7%; Pred. No. 3.8e+02;
RESULT 1495
ID ABL29667 standard; DNA; 2463 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 40474.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 30.4; DB 4; Length 2463;
Best Local Similarity 53.3%; Pred. No. 3.8e+02;

RESULT 1496
ID ADQ63910 standard; cDNA; 3113 BP.
DE Novel human cDNA sequence #1071.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.4%; Score 30.4; DB 12; Length 3113;
Best Local Similarity 50.7%; Pred. No. 4.3e+02;
RESULT 1497
ID ACN40680 standard; cDNA; 3781 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326760, SEQ ID NO:5610.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.4%; Score 30.4; DB 13; Length 3781;
Best Local Similarity 57.3%; Pred. No. 4.8e+02;
RESULT 1498
ID ADI02662 standard; cDNA; 4638 BP.
DE Human cDNA differentially expressed in the vascular endothelium #203.
PN US2003166903-A1.
PD 04-SEP-2003.
PA (ASTR/) ASTROMOFF A.
PA (BAND/) BANDMAN O.
PA (COCK/) COCKS B G.
Query Match 3.4%; Score 30.4; DB 10; Length 4638;
Best Local Similarity 57.3%; Pred. No. 5.4e+02;
RESULT 1499
ID AAL06099 standard; DNA; 6598 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8787.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.4; DB 4; Length 6598;
Best Local Similarity 52.3%; Pred. No. 6.5e+02;
RESULT 1500
ID ABL98664 standard; DNA; 6598 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3316.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 30.4; DB 4; Length 6598;
Best Local Similarity 52.3%; Pred. No. 6.5e+02;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 21:03:28 ; Search time 4898 Seconds
(without alignments)
6916.537 Million cell updates/sec

Title: US-10-036-214-60
Perfect score: 890
Sequence: 1 aagtacttgtgtccgggtgg.....taaaaaaaaaaatcatcaaa 890

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	833.2	93.6	874	3	AY037148	Homo sapi
c	2	655	73.6	716	5	BU682658	BU682658 UI-CF-EC1
	3	646.8	72.7	749	4	BG545668	BG545668 602572933
c	4	637	71.6	685	5	BU682973	BU682973 UI-CF-EC1
c	5	631.4	70.9	681	5	BU683324	BU683324 UI-CF-EC1
c	6	620	69.7	663	5	BU731651	BU731651 UI-E-CI1-
	7	616	69.2	796	4	BG203405	RST22786
c	8	615.8	69.2	729	6	CD370545	CD370545 UI-H-FT1-
c	9	602	67.6	660	5	BU678191	BU678191 UI-CF-EC0
c	10	598.6	67.3	621	6	CA440136	CA440136 UI-H-DT1-
	11	584	65.6	603	2	BF852989	BF852989 MR2-EN009
c	12	576	64.7	620	5	BU680465	BU680465 UI-CF-EC1
	13	573	64.4	581	5	BP216854	BP216854 BP216854
c	14	572.8	64.4	624	5	BM984582	BM984582 UI-CF-EC1
	15	556.6	62.5	582	5	BP316275	BP316275 BP316275
	16	550.8	61.9	563	2	BF852995	BF852995 MR2-EN009
	17	548.6	61.6	581	5	BP315987	BP315987 BP315987
	18	548.2	61.6	558	2	BF853000	BF853000 MR2-EN009
c	19	535	60.1	547	1	AI816715	AI816715 wj43b08.x
c	20	535	60.1	547	1	AI857902	AI857902 wj68a01.x
	21	534	60.0	597	4	BI010796	BI010796 MR2-EN009
	22	516.6	58.0	627	4	BI010793	BI010793 MR2-EN009
c	23	515	57.9	523	2	BE044451	BE044451 ho45g08.x
	24	514.2	57.8	536	2	BF853928	BF853928 MR2-EN009
c	25	510.2	57.3	534	1	AI936064	AI936064 wo47h12.x
c	26	506.2	56.9	511	1	AA688029	AA688029 nv16e12.s
	27	503.8	56.6	564	2	BF854481	BF854481 MR2-EN009
c	28	488.4	54.9	552	1	AI218954	AI218954 qg72g08.x
	29	470.4	52.9	683	7	CF181020	CF181020 817812 MA
	30	467	52.5	478	4	BM694846	BM694846 UI-E-CI1-
	31	457.8	51.4	640	7	CF367029	CF367029 841745 MA
	32	451.6	50.7	499	2	BF853920	BF853920 MR2-EN009
c	33	447.2	50.2	755	7	CK778328	CK778328 965485 MA
c	34	444.6	50.0	459	2	AW975331	AW975331 EST387439
c	35	443.6	49.8	457	1	AA192427	AA192427 zq01g08.s
	36	442.4	49.7	532	2	BF846558	BF846558 QV0-EN005
	37	442.4	49.7	532	5	BQ329985	BQ329985 QV0-EN005
	38	437.8	49.2	543	4	BI010755	BI010755 MR2-EN009
	39	429.8	48.3	690	7	CK981586	CK981586 4114137 B
c	40	427.2	48.0	464	2	BF846063	BF846063 QV0-EN005
	41	423.4	47.6	605	7	CF793784	CF793784 889229 MA
	42	417	46.9	445	1	AJ572670	AJ572670 AJ572670
c	43	410	46.1	467	2	BF846065	BF846065 QV0-EN005
	44	408	45.8	463	2	BF848191	BF848191 QV0-EN005
	45	406.8	45.7	463	2	BF848190	BF848190 QV0-EN005
	46	400.2	45.0	452	7	W37255	W37255 zc09f01.r1
	47	400	44.9	462	2	BF846059	BF846059 QV0-EN005
	48	399.8	44.9	517	7	CF359042	CF359042 818670 MA
c	49	398.4	44.8	400	1	AA661735	AA661735 nv04b11.s
	50	394.2	44.3	407	2	BF853537	BF853537 MR2-EN009
	51	388.4	43.6	423	7	F28028	F28028 HSPD16404 H
	52	383.2	43.1	451	7	W32197	W32197 zc04f05.r1
c	53	381.4	42.9	579	7	CF359576	CF359576 820836 MA
c	54	375.4	42.2	558	7	CF368434	CF368434 853081 MA
	55	372.4	41.8	576	7	CV347722	CV347722 MR2-EN009
c	56	368.4	41.4	624	7	CK940308	CK940308 4113753 B
c	57	366.4	41.2	412	1	AA854779	AA854779 aj77b05.s
	58	363.8	40.9	402	7	F33888	F33888 HSPD28217 H
	59	363	40.8	395	7	F20527	F20527 HSPD04880 H
c	60	363	40.8	420	5	BQ184690	BQ184690 UI-E-EJ1-
	61	363	40.8	779	5	BQ186119	BQ186119 UI-E-EJ1-
c	62	362.8	40.8	440	1	AA903899	AA903899 oe78e07.s
	63	362.4	40.7	475	5	BX116627	BX116627 BX116627
	64	359.2	40.4	568	6	CB421055	CB421055 594052 MA
	65	356.2	40.0	436	7	F36903	F36903 HSPD34824 H
	66	354	39.8	712	4	BG716603	BG716603 602677864
	67	353.6	39.7	463	2	BF848198	BF848198 QV0-EN005
	68	350.6	39.4	430	1	AA192426	AA192426 zq01g08.r
c	69	338.4	38.0	573	4	BM189978	BM189978 POSM01000
	70	336	37.8	789	4	BG483879	BG483879 602504455
	71	332.8	37.4	336	1	AJ711977	AJ711977 AJ711977
c	72	330	37.1	352	7	H83927	H83927 ys64b02.s1
	73	329	37.0	548	4	BG740933	BG740933 602634538
c	74	324	36.4	437	7	W33189	W33189 zc09f01.s1
	75	320	36.0	334	7	F24489	F24489 HSPD10829 H
c	76	319	35.8	547	6	CB420692	CB420692 593668 MA
c	77	310.4	34.9	316	1	AI382922	AI382922 tc20e03.x
	78	296.4	33.3	543	7	CK979926	CK979926 4111634 B
c	79	288.4	32.4	298	1	AI659751	AI659751 tt97h09.x
	80	287.8	32.3	440	7	H83784	H83784 ys64b02.r1
	81	285	32.0	331	7	F25113	F25113 HSPD11902 H
	82	275.2	30.9	280	7	F26660	F26660 HSPD14219 H
	83	272.8	30.7	277	7	F19507	F19507 HSPD04111 H
c	84	271	30.4	314	1	AA902491	AA902491 ok91h01.s
	85	270	30.3	558	4	BM538776	BM538776 ha99f12.g
	86	264.2	29.7	514	7	CF614718	CF614718 CES009101
c	87	260	29.2	400	7	CF792426	CF792426 885357 MA
c	88	258.4	29.0	400	7	CN070415	CN070415 858166 MA
	89	257.8	29.0	454	2	BF890431	BF890431 292000 MA
	90	254.2	28.6	591	6	CD287842	CD287842 1_M6.abd
	91	253.2	28.4	401	2	BE165776	BE165776 CM3-HT048
c	92	250.2	28.1	293	1	AI863957	AI863957 wj54a02.x
c	93	250	28.1	310	4	BG214764	BG214764 RST34418
	94	245.8	27.6	1048	3	AK006964	AK006964 Mus muscu
	95	244.4	27.5	258	7	F31628	F31628 HSPD22948 H
	96	240.8	27.1	561	1	AI546994	AI546994 PN2.1_12_
	97	232.8	26.2	260	7	F26233	F26233 HSPD13635 H

	98	226.4	25.4	413	2	BF599823	BF599823 264147 MA
	99	225.8	25.4	301	4	BI848187	BI848187 470542 MA
	100	224.8	25.3	242	2	BF853580	BF853580 MR2-EN009
c	101	221.8	24.9	257	5	BQ329874	BQ329874 QV0-EN005
	102	219.8	24.7	270	7	F26013	F26013 HSPD13279 H
c	103	205.4	23.1	427	1	AI124773	AI124773 am56a04.x
c	104	194.4	21.8	283	1	AA661823	AA661823 nv05a11.s
c	105	189.6	21.3	229	7	W32232	W32232 zc04f05.s1
	106	186	20.9	581	7	CF104379	CF104379 maj31g09.
c	107	175.2	19.7	444	7	CK979689	CK979689 4111250 B
c	108	175	19.7	308	2	BF846130	BF846130 QV0-EN005
	109	171	19.2	529	6	CB453250	CB453250 708210 MA
c	110	170.8	19.2	385	6	CB168825	CB168825 CWI602769
	111	165	18.5	352	2	AW327171	AW327171 20827 MAR
	112	159.6	17.9	271	2	AW607505	AW607505 CM3-HT048
c	113	153.4	17.2	155	1	AA194737	AA194737 zq07e03.s
	114	152.8	17.2	174	5	BQ329966	BQ329966 MR2-EN009
	115	144.6	16.2	637	6	BY707018	BY707018 BY707018
	116	142.2	16.0	604	6	CB274851	CB274851 mai74f08.
c	117	132	14.8	276	1	AI326322	AI326322 ml57e12.x
	118	125.6	14.1	762	5	BU262229	BU262229 603374147
	119	122.8	13.8	556	5	BX521337	BX521337 BX521337
	120	122.6	13.8	810	5	BU375412	BU375412 603812633
	121	121.6	13.7	613	1	AA064422	AA064422 ml48h01.r
	122	120.8	13.6	558	1	AI046571	AI046571 uh27d09.r
	123	120	13.5	539	1	AI386005	AI386005 ml57e12.y
c	124	113.8	12.8	262	8	AQ350175	AQ350175 RPCI11-11
c	125	113.8	12.8	385	8	AQ629868	AQ629868 RPCI-11-4
	126	112	12.6	642	4	BI390206	BI390206 pgp1c.pk0
	127	108	12.1	708	7	CK806751	CK806751 AGENCOURT
	128	108	12.1	709	7	CK806762	CK806762 AGENCOURT
c	129	108	12.1	745	7	CN318344	CN318344 AGENCOURT
	130	108	12.1	755	7	CK804240	CK804240 AGENCOURT
	131	106.6	12.0	449	5	BU936490	BU936490 AGENCOURT
c	132	98	11.0	867	6	CB564543	CB564543 AGENCOURT
	133	97.8	11.0	832	7	CF590685	CF590685 AGENCOURT
	134	97.2	10.9	749	7	CN833130	CN833130 AGENCOURT
	135	94.8	10.7	796	7	CK806660	CK806660 AGENCOURT
	136	94.8	10.7	843	6	CD302397	CD302397 AGENCOURT
c	137	94.8	10.7	878	7	CV116535	CV116535 AGENCOURT
c	138	93.6	10.5	638	6	CB454117	CB454117 710818 MA
	139	81.2	9.1	759	7	CV078885	CV078885 AGENCOURT
	140	81	9.1	545	7	CK234584	CK234584 SB0100110
	141	80.6	9.1	680	6	BY706735	BY706735 BY706735
	142	80.6	9.1	717	3	AK006750	AK006750 Mus muscu
	143	80.6	9.1	825	5	BU962223	BU962223 AGENCOURT
	144	78.6	8.8	553	8	AZ814026	AZ814026 2M0081L06
	145	76.8	8.6	426	2	BF021921	BF021921 uy59g01.y
	146	73.4	8.2	847	5	BU316742	BU316742 603849530
	147	73	8.2	877	6	CB201351	CB201351 AGENCOURT
	148	67.8	7.6	869	5	BU377285	BU377285 603812859
	149	62.2	7.0	551	7	CN807765	CN807765 HDAH11B02
	150	59	6.6	372	4	BI299045	BI299045 UI-R-CV2-
	151	59	6.6	402	4	BI298876	BI298876 UI-R-CV2-
	152	59	6.6	424	4	BG373709	BG373709 UI-R-CV1-
	153	59	6.6	476	1	AA893763	AA893763 EST197566
	154	59	6.6	485	4	BI300958	BI300958 UI-R-CV2-
	155	59	6.6	548	2	BF287672	BF287672 EST452263
	156	56.8	6.4	551	7	CV039031	CV039031 4136331 B
	157	56.2	6.3	726	7	CV508675	CV508675 kc74g12.y
	158	53.4	6.0	355	4	BI299389	BI299389 UI-R-CV2-
	159	52	5.8	598	5	BQ692121	BQ692121 pt03b07.y
	160	51.2	5.8	520	2	BE602964	BE602964 HVSMEh010
c	161	51	5.7	384	8	AZ784977	AZ784977 2M0028J20
	162	50.4	5.7	557	5	BQ739132	BQ739132 pt40g03.y
	163	50.4	5.7	574	5	BQ739081	BQ739081 pt40b03.y
	164	50.4	5.7	582	5	BQ738778	BQ738778 pt20e08.y
	165	50.4	5.7	689	5	BX618342	BX618342 BX618342
c	166	50.4	5.7	978	3	CNS08P6L	BX022057 Single re
	167	49.6	5.6	583	6	CD681976	CD681976 rj22c09.y
	168	49.6	5.6	691	6	CD683218	CD683218 rj40g09.y
	169	49.6	5.6	967	3	CNS08VJ7	BX030287 Single re
	170	49.4	5.6	641	4	BI594431	BI594431 As_nc_12H
	171	49	5.5	532	2	AW871321	AW871321 ra75g05.y
	172	48.8	5.5	576	5	BQ692487	BQ692487 pt15e05.y
c	173	48.8	5.5	825	3	CNS08VJ8	BX030288 Single re
	174	48	5.4	709	7	CF801907	CF801907 rj54b07.y
	175	47.8	5.4	478	7	CV127621	CV127621 CSEQSDA01
	176	47.8	5.4	602	4	BM280695	BM280695 ki03h11.y
	177	47.8	5.4	712	6	CB040158	CB040158 As_L3_47A
	178	47.8	5.4	714	6	CB039831	CB039831 As_L3_41G
	179	47.8	5.4	1117	7	CK208964	CK208964 FGAS02069
	180	47.4	5.3	570	4	BG520804	BG520804 ps51h10.y
	181	47.2	5.3	592	5	BQ738312	BQ738312 pt30e12.y
	182	47.2	5.3	595	5	BQ738675	BQ738675 pt19d01.y
	183	47.2	5.3	612	6	CA297966	CA297966 SCCCSD1C0
	184	47.2	5.3	685	6	CA284643	CA284643 SCSFSD106
	185	47	5.3	431	6	CB757895	CB757895 AMGNNUC:N
	186	47	5.3	540	6	CB612856	CB612856 AMGNNUC:N
	187	47	5.3	560	6	CB609739	CB609739 AMGNNUC:N
	188	47	5.3	573	6	CB615133	CB615133 AMGNNUC:N
	189	47	5.3	585	6	CB585928	CB585928 AMGNNUC:N
	190	47	5.3	595	6	CB584086	CB584086 AMGNNUC:N
	191	47	5.3	602	6	CB582179	CB582179 AMGNNUC:N
	192	47	5.3	604	6	CB581793	CB581793 AMGNNUC:N
	193	47	5.3	624	6	CB578332	CB578332 AMGNNUC:N
	194	47	5.3	641	6	CA338375	CA338375 NISC_1x02
	195	47	5.3	665	7	CF979423	CF979423 F23A03_03
	196	47	5.3	717	7	CK471814	CK471814 AGENCOURT
	197	47	5.3	722	6	CD372873	CD372873 UI-R-GR0-
	198	47	5.3	755	7	CO573897	CO573897 AGENCOURT
	199	47	5.3	764	6	CD372844	CD372844 UI-R-GR0-
	200	46.8	5.3	591	5	BQ737887	BQ737887 pt24h07.y
	201	46.4	5.2	456	6	CB740595	CB740595 AMGNNUC:N
	202	46.4	5.2	514	6	CB716787	CB716787 AMGNNUC:N
	203	46.4	5.2	580	7	CO575405	CO575405 AGENCOURT
	204	46.4	5.2	1168	3	AY111549	AY111549 Zea mays
	205	46.2	5.2	191	7	CK970994	CK970994 4086608 B
	206	46.2	5.2	580	6	CD891537	CD891537 G118.117K
	207	46.2	5.2	685	7	CN011333	CN011333 WHE3882_H
c	208	46.2	5.2	687	6	CD891538	CD891538 G118.117K
	209	46	5.2	544	6	CB612093	CB612093 AMGNNUC:N
	210	46	5.2	588	6	CB585191	CB585191 AMGNNUC:N
	211	45.8	5.1	581	2	AW827975	AW827975 ra60b09.y
	212	45.4	5.1	514	4	BG664684	BG664684 DRABHE10
	213	45.4	5.1	583	6	CB586311	CB586311 AMGNNUC:N
	214	45.4	5.1	688	6	CB556583	CB556583 AMGNNUC:C
	215	45.2	5.1	294	9	CG483783	CG483783 OST17529
	216	45.2	5.1	583	4	BM653074	BM653074 170006873
	217	44.8	5.0	482	6	CB728014	CB728014 AMGNNUC:C
	218	44.8	5.0	529	5	BM986300	BM986300 EST531208
	219	44.6	5.0	470	7	CK983530	CK983530 re26a12.y
	220	44.4	5.0	558	9	CL965962	CL965962 OsIFCC013
	221	44.2	5.0	271	7	CO412467	CO412467 EST842852
	222	44.2	5.0	293	9	CG485857	CG485857 OST20501
	223	44.2	5.0	293	9	CG486312	CG486312 OST21223
	224	44.2	5.0	320	7	CV136417	CV136417 EST847626
	225	44.2	5.0	339	9	CL971647	CL971647 OsIFCC021
	226	44.2	5.0	437	7	CV138791	CV138791 EST850000
	227	44.2	5.0	453	7	CV137383	CV137383 EST848592
	228	44.2	5.0	482	7	CV139363	CV139363 EST850572
	229	44.2	5.0	491	6	CB887459	CB887459 Lice_01_B
	230	44.2	5.0	562	7	CO412208	CO412208 EST842593
	231	44.2	5.0	563	7	CV141158	CV141158 EST852367
	232	44.2	5.0	568	7	CO409403	CO409403 EST839788
	233	44.2	5.0	580	7	CV135289	CV135289 EST846498
	234	44.2	5.0	584	7	CR537007	CR537007 DKFZp459B
	235	44.2	5.0	594	7	CO412173	CO412173 EST842558
	236	44.2	5.0	594	7	CO413169	CO413169 EST843554
	237	44.2	5.0	595	7	CO411962	CO411962 EST842347
c	238	44.2	5.0	607	7	CV134440	CV134440 EST845649
	239	44.2	5.0	612	7	CV142492	CV142492 EST853701
c	240	44.2	5.0	613	7	CV134227	CV134227 EST845436
	241	44.2	5.0	615	7	CO410230	CO410230 EST840615
c	242	44.2	5.0	620	7	CV134297	CV134297 EST845506
	243	44.2	5.0	622	7	CO414258	CO414258 EST844643

c	244	44.2	5.0	671	7	CV134491	CV134491 EST845700		317	44.2	5.0	803	7	CO410893	CO410893 EST841278	
	245	44.2	5.0	673	7	CV149400	CV149400 EST860610		318	44.2	5.0	803	7	CV142699	CV142699 EST853908	
c	246	44.2	5.0	682	7	CV134462	CV134462 EST845671		319	44.2	5.0	804	7	CO413074	CO413074 EST843459	
	247	44.2	5.0	685	7	CN784825	CN784825 EST783516		320	44.2	5.0	805	7	CN784974	CN784974 EST783665	
	248	44.2	5.0	688	7	CO413232	CO413232 EST843617		321	44.2	5.0	805	7	CV133883	CV133883 EST845092	
	249	44.2	5.0	689	7	CV136775	CV136775 EST847984		322	44.2	5.0	806	7	CO410126	CO410126 EST840511	
	250	44.2	5.0	701	7	CN785851	CN785851 EST784542		323	44.2	5.0	807	7	CN784506	CN784506 EST783197	
	251	44.2	5.0	705	7	CV141318	CV141318 EST852527		324	44.2	5.0	807	7	CN785488	CN785488 EST784179	
	252	44.2	5.0	714	7	CV134648	CV134648 EST845857		325	44.2	5.0	807	7	CO410196	CO410196 EST840581	
	253	44.2	5.0	732	7	CV135358	CV135358 EST846567		326	44.2	5.0	807	7	CV137474	CV137474 EST848683	
	254	44.2	5.0	736	7	CV142857	CV142857 EST854066		327	44.2	5.0	808	7	CO411044	CO411044 EST841429	
	255	44.2	5.0	738	7	CO414566	CO414566 EST844951		328	44.2	5.0	809	7	CO411447	CO411447 EST841832	
	256	44.2	5.0	739	7	CV145581	CV145581 EST856790		329	44.2	5.0	809	7	CV149500	CV149500 EST860710	
	257	44.2	5.0	742	7	CO411549	CO411549 EST841934		330	44.2	5.0	810	7	CV141123	CV141123 EST852332	
	258	44.2	5.0	743	7	CV149242	CV149242 EST860451		331	44.2	5.0	810	7	CV143466	CV143466 EST854675	
	259	44.2	5.0	749	7	CN785523	CN785523 EST784214		332	44.2	5.0	810	7	CV149105	CV149105 EST860314	
	260	44.2	5.0	749	7	CV140967	CV140967 EST852176		333	44.2	5.0	811	7	CO411280	CO411280 EST841665	
	261	44.2	5.0	751	4	BM617788	BM617788 170006871		334	44.2	5.0	811	7	CV136901	CV136901 EST848110	
	262	44.2	5.0	751	7	CV134566	CV134566 EST845775		335	44.2	5.0	811	7	CV142578	CV142578 EST853787	
	263	44.2	5.0	751	7	CV138952	CV138952 EST850161		336	44.2	5.0	811	7	CV144803	CV144803 EST856012	
	264	44.2	5.0	751	7	CV149269	CV149269 EST860478		337	44.2	5.0	812	7	CO413580	CO413580 EST843965	
	265	44.2	5.0	752	7	CN785811	CN785811 EST784502		338	44.2	5.0	812	7	CO414007	CO414007 EST844392	
c	266	44.2	5.0	755	7	CN783590	CN783590 EST782281		339	44.2	5.0	812	7	CV145455	CV145455 EST856664	
	267	44.2	5.0	755	7	CO409004	CO409004 EST839389		340	44.2	5.0	812	7	CV145529	CV145529 EST856738	
	268	44.2	5.0	755	7	CV138473	CV138473 EST849682		341	44.2	5.0	813	7	CO413644	CO413644 EST844029	
	269	44.2	5.0	759	7	CV140558	CV140558 EST851767		342	44.2	5.0	813	7	CV143848	CV143848 EST855057	
	270	44.2	5.0	761	7	CN784722	CN784722 EST783413		343	44.2	5.0	814	7	CN784173	CN784173 EST782864	
	271	44.2	5.0	767	7	CO413088	CO413088 EST843473		344	44.2	5.0	814	7	CV135422	CV135422 EST846631	
	272	44.2	5.0	767	7	CV138483	CV138483 EST849692		345	44.2	5.0	814	7	CV136068	CV136068 EST847277	
	273	44.2	5.0	767	7	CV139190	CV139190 EST850399		346	44.2	5.0	814	7	CV139846	CV139846 EST851055	
	274	44.2	5.0	768	7	CO414230	CO414230 EST844615		347	44.2	5.0	814	7	CV141343	CV141343 EST852552	
	275	44.2	5.0	769	7	CN784518	CN784518 EST783209		348	44.2	5.0	814	7	CV145111	CV145111 EST856320	
	276	44.2	5.0	769	7	CV135845	CV135845 EST847054		349	44.2	5.0	815	7	CN784797	CN784797 EST783488	
	277	44.2	5.0	769	7	CV136518	CV136518 EST847727		350	44.2	5.0	815	7	CN785062	CN785062 EST783753	
	278	44.2	5.0	769	7	CV136829	CV136829 EST848038		351	44.2	5.0	815	7	CO412610	CO412610 EST842995	
	279	44.2	5.0	769	7	CV144094	CV144094 EST855303		352	44.2	5.0	815	7	CV138377	CV138377 EST849586	
	280	44.2	5.0	770	7	CO411485	CO411485 EST841870		353	44.2	5.0	815	7	CV140836	CV140836 EST852045	
	281	44.2	5.0	770	7	CV136579	CV136579 EST847788		354	44.2	5.0	815	7	CV142218	CV142218 EST853427	
	282	44.2	5.0	771	7	CV136707	CV136707 EST847916		355	44.2	5.0	815	7	CV142393	CV142393 EST853602	
	283	44.2	5.0	771	7	CV141681	CV141681 EST852890		356	44.2	5.0	815	7	CV143594	CV143594 EST854803	
	284	44.2	5.0	772	7	CN784164	CN784164 EST782855		357	44.2	5.0	816	7	CO410418	CO410418 EST840803	
	285	44.2	5.0	777	7	CO409874	CO409874 EST840259		358	44.2	5.0	816	7	CO411127	CO411127 EST841512	
	286	44.2	5.0	777	7	CO411729	CO411729 EST842114		359	44.2	5.0	816	7	CO412865	CO412865 EST843250	
	287	44.2	5.0	777	7	CO411784	CO411784 EST842169		360	44.2	5.0	816	7	CV135415	CV135415 EST846624	
	288	44.2	5.0	777	7	CO411816	CO411816 EST842201		361	44.2	5.0	816	7	CV135750	CV135750 EST846959	
	289	44.2	5.0	777	7	CO412744	CO412744 EST843129		362	44.2	5.0	816	7	CV140508	CV140508 EST851717	
	290	44.2	5.0	777	7	CV136726	CV136726 EST847935		363	44.2	5.0	816	7	CV141138	CV141138 EST852347	
	291	44.2	5.0	780	7	CV147766	CV147766 EST858975		364	44.2	5.0	816	7	CV141545	CV141545 EST852754	
	292	44.2	5.0	781	7	CO413883	CO413883 EST844268		365	44.2	5.0	816	7	CV144409	CV144409 EST855618	
	293	44.2	5.0	782	7	CO410325	CO410325 EST840710		366	44.2	5.0	816	7	CV149636	CV149636 EST860846	
	294	44.2	5.0	783	7	CO409065	CO409065 EST839450		367	44.2	5.0	817	7	CN784552	CN784552 EST783243	
	295	44.2	5.0	783	7	CO409477	CO409477 EST839862		368	44.2	5.0	817	7	CN785541	CN785541 EST784232	
	296	44.2	5.0	783	7	CO410085	CO410085 EST840470		369	44.2	5.0	817	7	CN785796	CN785796 EST784487	
	297	44.2	5.0	783	7	CV139239	CV139239 EST850448		370	44.2	5.0	817	7	CO409993	CO409993 EST840378	
	298	44.2	5.0	783	7	CV139718	CV139718 EST850927		371	44.2	5.0	817	7	CO410580	CO410580 EST840965	
	299	44.2	5.0	786	7	CV145430	CV145430 EST856639		372	44.2	5.0	817	7	CO411010	CO411010 EST841395	
	300	44.2	5.0	787	7	CO414340	CO414340 EST844725		373	44.2	5.0	817	7	CO412561	CO412561 EST842946	
	301	44.2	5.0	787	7	CV138763	CV138763 EST849972		374	44.2	5.0	817	7	CO414582	CO414582 EST844967	
	302	44.2	5.0	787	7	CV143795	CV143795 EST855004		375	44.2	5.0	817	7	CV136745	CV136745 EST847954	
	303	44.2	5.0	788	7	CV145750	CV145750 EST856959		376	44.2	5.0	817	7	CV138824	CV138824 EST850033	
	304	44.2	5.0	789	7	CN783589	CN783589 EST782280		377	44.2	5.0	817	7	CV139197	CV139197 EST850406	
	305	44.2	5.0	793	7	CO410528	CO410528 EST840913		378	44.2	5.0	817	7	CV141505	CV141505 EST852714	
	306	44.2	5.0	793	7	CO410700	CO410700 EST841085		379	44.2	5.0	817	7	CV142056	CV142056 EST853265	
	307	44.2	5.0	793	7	CR769293	CR769293 DKFZp469C		380	44.2	5.0	817	7	CV142361	CV142361 EST853570	
	308	44.2	5.0	793	7	CV135425	CV135425 EST846634		381	44.2	5.0	817	7	CV142537	CV142537 EST853746	
	309	44.2	5.0	794	7	CV135620	CV135620 EST846829		382	44.2	5.0	817	7	CV145072	CV145072 EST856281	
	310	44.2	5.0	795	7	CN783492	CN783492 EST782183		383	44.2	5.0	817	7	CV146190	CV146190 EST857399	
	311	44.2	5.0	795	7	CN785554	CN785554 EST784245		384	44.2	5.0	817	7	CV147633	CV147633 EST858842	
	312	44.2	5.0	797	7	CO412131	CO412131 EST842516		385	44.2	5.0	818	7	CO410537	CO410537 EST840922	
	313	44.2	5.0	800	7	CN785345	CN785345 EST784036		386	44.2	5.0	818	7	CO414299	CO414299 EST844684	
	314	44.2	5.0	801	7	CO413945	CO413945 EST844330		387	44.2	5.0	818	7	CV134907	CV134907 EST846116	
	315	44.2	5.0	802	7	CO410240	CO410240 EST840625		388	44.2	5.0	818	7	CV143279	CV143279 EST854488	
	316	44.2	5.0	802	7	CO410291	CO410291 EST840676		389	44.2	5.0	818	7	CV144341	CV144341 EST855550	

390	44.2	5.0	818	7	CV144973	CV144973	EST856182
391	44.2	5.0	819	7	CN783786	CN783786	EST782477
392	44.2	5.0	819	7	CN784736	CN784736	EST783427
393	44.2	5.0	820	7	CO413811	CO413811	EST844196
394	44.2	5.0	820	7	CV147900	CV147900	EST859109
395	44.2	5.0	820	7	CV149317	CV149317	EST860526
396	44.2	5.0	821	7	CV134881	CV134881	EST846090
397	44.2	5.0	821	7	CV139161	CV139161	EST850370
398	44.2	5.0	822	7	CO413555	CO413555	EST843940
399	44.2	5.0	822	7	CO413643	CO413643	EST844028
400	44.2	5.0	823	7	CO409789	CO409789	EST840174
401	44.2	5.0	823	7	CO414517	CO414517	EST844902
402	44.2	5.0	823	7	CV136544	CV136544	EST847753
403	44.2	5.0	823	7	CV140854	CV140854	EST852063
404	44.2	5.0	823	7	CV145532	CV145532	EST856741
405	44.2	5.0	824	7	CO410675	CO410675	EST841060
406	44.2	5.0	824	7	CO410781	CO410781	EST841166
407	44.2	5.0	824	7	CO411330	CO411330	EST841715
408	44.2	5.0	824	7	CO412839	CO412839	EST843224
409	44.2	5.0	824	7	CV135603	CV135603	EST846812
410	44.2	5.0	824	7	CV138560	CV138560	EST849769
411	44.2	5.0	824	7	CV138884	CV138884	EST850093
412	44.2	5.0	824	7	CV139785	CV139785	EST850994
413	44.2	5.0	824	7	CV145814	CV145814	EST857023
414	44.2	5.0	825	7	CO409340	CO409340	EST839725
415	44.2	5.0	825	7	CO409910	CO409910	EST840295
416	44.2	5.0	825	7	CO410082	CO410082	EST840467
417	44.2	5.0	825	7	CV135728	CV135728	EST846937
418	44.2	5.0	825	7	CV137682	CV137682	EST848891
419	44.2	5.0	825	7	CV144549	CV144549	EST855758
420	44.2	5.0	826	7	CO409656	CO409656	EST840041
421	44.2	5.0	826	7	CV139020	CV139020	EST850229
422	44.2	5.0	827	7	CN783897	CN783897	EST782588
423	44.2	5.0	827	7	CN785602	CN785602	EST784293
424	44.2	5.0	827	7	CO413960	CO413960	EST844345
425	44.2	5.0	827	7	CO414001	CO414001	EST844386
426	44.2	5.0	827	7	CO414424	CO414424	EST844809
427	44.2	5.0	827	7	CV142605	CV142605	EST853814
428	44.2	5.0	828	7	CO413184	CO413184	EST843569
429	44.2	5.0	828	7	CO413486	CO413486	EST843871
430	44.2	5.0	828	7	CV133868	CV133868	EST845077
431	44.2	5.0	828	7	CV136313	CV136313	EST847522
432	44.2	5.0	829	7	CO413529	CO413529	EST843914
433	44.2	5.0	829	7	CV138554	CV138554	EST849763
434	44.2	5.0	829	7	CV142487	CV142487	EST853696
435	44.2	5.0	830	7	CN783666	CN783666	EST782357
436	44.2	5.0	830	7	CO411555	CO411555	EST841940
437	44.2	5.0	830	7	CO413071	CO413071	EST843456
438	44.2	5.0	830	7	CV138877	CV138877	EST850086
439	44.2	5.0	830	7	CV147446	CV147446	EST858655
440	44.2	5.0	830	7	CV148019	CV148019	EST859228
441	44.2	5.0	831	7	CV147360	CV147360	EST858569
442	44.2	5.0	831	7	CV148822	CV148822	EST860031
443	44.2	5.0	832	7	CO411104	CO411104	EST841489
444	44.2	5.0	832	7	CO413793	CO413793	EST844178
445	44.2	5.0	832	7	CO414105	CO414105	EST844490
446	44.2	5.0	832	7	CV136106	CV136106	EST847315
447	44.2	5.0	832	7	CV138630	CV138630	EST849839
448	44.2	5.0	832	7	CV145391	CV145391	EST856600
449	44.2	5.0	833	7	CN785645	CN785645	EST784336
450	44.2	5.0	833	7	CO409180	CO409180	EST839565
451	44.2	5.0	833	7	CO409763	CO409763	EST840148
452	44.2	5.0	833	7	CO409925	CO409925	EST840310
453	44.2	5.0	833	7	CO410931	CO410931	EST841316
454	44.2	5.0	833	7	CO412235	CO412235	EST842620
455	44.2	5.0	833	7	CO412791	CO412791	EST843176
456	44.2	5.0	833	7	CV134679	CV134679	EST845888
457	44.2	5.0	833	7	CV135155	CV135155	EST846364
458	44.2	5.0	833	7	CV136263	CV136263	EST847472
459	44.2	5.0	833	7	CV138964	CV138964	EST850173
460	44.2	5.0	833	7	CV139038	CV139038	EST850247
461	44.2	5.0	833	7	CV139085	CV139085	EST850294
462	44.2	5.0	833	7	CV140076	CV140076	EST851285
463	44.2	5.0	833	7	CV142356	CV142356	EST853565
464	44.2	5.0	834	7	CO408944	CO408944	EST839329
465	44.2	5.0	834	7	CO411351	CO411351	EST841736
466	44.2	5.0	834	7	CO411366	CO411366	EST841751
467	44.2	5.0	834	7	CO412750	CO412750	EST843135
468	44.2	5.0	834	7	CV135023	CV135023	EST846232
469	44.2	5.0	834	7	CV136043	CV136043	EST847252
470	44.2	5.0	834	7	CV138607	CV138607	EST849816
471	44.2	5.0	834	7	CV142325	CV142325	EST853534
472	44.2	5.0	834	7	CV143851	CV143851	EST855060
473	44.2	5.0	834	7	CV144247	CV144247	EST855456
474	44.2	5.0	835	7	CN784073	CN784073	EST782764
475	44.2	5.0	835	7	CN784853	CN784853	EST783544
476	44.2	5.0	835	7	CN786012	CN786012	EST784703
477	44.2	5.0	835	7	CO409346	CO409346	EST839731
478	44.2	5.0	835	7	CO409559	CO409559	EST839944
479	44.2	5.0	835	7	CO411651	CO411651	EST842036
480	44.2	5.0	835	7	CO411822	CO411822	EST842207
481	44.2	5.0	835	7	CO412112	CO412112	EST842497
482	44.2	5.0	835	7	CO412668	CO412668	EST843053
483	44.2	5.0	835	7	CO412671	CO412671	EST843056
484	44.2	5.0	835	7	CO412813	CO412813	EST843198
485	44.2	5.0	835	7	CO413223	CO413223	EST843608
486	44.2	5.0	835	7	CO413729	CO413729	EST844114
487	44.2	5.0	835	7	CO414535	CO414535	EST844920
488	44.2	5.0	835	7	CV134055	CV134055	EST845264
489	44.2	5.0	835	7	CV138816	CV138816	EST850025
490	44.2	5.0	835	7	CV139803	CV139803	EST851012
491	44.2	5.0	835	7	CV142504	CV142504	EST853713
492	44.2	5.0	835	7	CV142999	CV142999	EST854208
493	44.2	5.0	835	7	CV147255	CV147255	EST858464
494	44.2	5.0	835	7	CV147339	CV147339	EST858548
495	44.2	5.0	835	7	CV148621	CV148621	EST859830
496	44.2	5.0	836	7	CN783946	CN783946	EST782637
497	44.2	5.0	836	7	CO411024	CO411024	EST841409
498	44.2	5.0	836	7	CV136952	CV136952	EST848161
499	44.2	5.0	836	7	CV145049	CV145049	EST856258
500	44.2	5.0	836	7	CV145845	CV145845	EST857054
501	44.2	5.0	838	7	CN784810	CN784810	EST783501
502	44.2	5.0	838	7	CV143399	CV143399	EST854608
503	44.2	5.0	838	7	CV143682	CV143682	EST854891
504	44.2	5.0	838	7	CV149577	CV149577	EST860787
505	44.2	5.0	839	7	CV137991	CV137991	EST849200
506	44.2	5.0	840	7	CN784155	CN784155	EST782846
507	44.2	5.0	849	7	CV135138	CV135138	EST846347
508	44.2	5.0	850	7	CV145419	CV145419	EST856628
509	44.2	5.0	851	7	CV143884	CV143884	EST855093
510	44.2	5.0	851	7	CV146099	CV146099	EST857308
511	44.2	5.0	860	7	CV144180	CV144180	EST855389
512	44.2	5.0	862	7	CO412376	CO412376	EST842761
513	44.2	5.0	863	7	CO412548	CO412548	EST842933
514	44.2	5.0	863	7	CV145833	CV145833	EST857042
515	44.2	5.0	870	7	CN785481	CN785481	EST784172
516	44.2	5.0	881	7	CN785528	CN785528	EST784219
517	44	4.9	596	2	AW152790	AW152790	JALsL3C04
518	44	4.9	647	2	AW152819	AW152819	JALsL3C15
519	43.8	4.9	523	6	CB214439	CB214439	OML04719
520	43.4	4.9	519	4	BM569421	BM569421	kj61a07.y
521	43.4	4.9	573	6	CA305060	CA305060	As_adfo_2
522	43.4	4.9	609	4	BM280647	BM280647	ki03d02.y
523	43.4	4.9	609	6	CA304376	CA304376	As_adfo_1
524	43.4	4.9	616	6	CA304387	CA304387	As_adfo_1
525	43.4	4.9	630	6	CA304189	CA304189	As_adfo_1
526	43.4	4.9	635	6	CA304762	CA304762	As_adfo_2
527	43.4	4.9	642	4	BM515899	BM515899	kj54g10.y
528	43.4	4.9	644	4	BM280607	BM280607	ki02h02.y
529	43.4	4.9	644	6	CA303663	CA303663	As_adfo_0
530	43.4	4.9	671	6	CA849832	CA849832	kl05h07.y
531	43.4	4.9	676	6	CB014919	CB014919	As_tgz_87
532	43.4	4.9	682	6	CB014521	CB014521	As_tgz_81
533	43.2	4.9	292	9	CG491092	CG491092	OST28437
534	43.2	4.9	437	1	AI815634	AI815634	au43d05.y
c 535	43.2	4.9	546	1	AI292478	AI292478	GH15391.3

	536	43.2	4.9	587	4	BI593007	BI593007 RH10864.5
	537	43.2	4.9	604	7	CK524922	CK524922 rswfa0_00
	538	43.2	4.9	612	4	BI625463	BI625463 RH6589I.5
	539	43.2	4.9	638	1	AI238451	AI238451 GH14494.5
	540	43	4.8	341	4	BM569376	BM569376 kj60d01.y
	541	43	4.8	463	4	BM517951	BM517951 ki84h01.y
	542	43	4.8	533	4	BM284014	BM284014 ki36f09.y
c	543	43	4.8	884	9	CNS006U0	AL065923 Drosophil
	544	42.8	4.8	263	2	AW312690	AW312690 4894 MARC
	545	42.8	4.8	275	7	CO261636	CO261636 4133938 B
	546	42.8	4.8	419	7	CN997982	CN997982 UMC-bcl_0
	547	42.8	4.8	423	1	AV665364	AV665364 AV665364
	548	42.8	4.8	470	1	AV592507	AV592507 AV592507
	549	42.8	4.8	554	1	AV600003	AV600003 AV600003
	550	42.8	4.8	562	5	BM967957	BM967957 LM24HW008
	551	42.8	4.8	650	7	CN792506	CN792506 4127376 B
	552	42.8	4.8	668	7	CK947480	CK947480 4072509 B
	553	42.8	4.8	696	7	CK982036	CK982036 4114314 B
	554	42.8	4.8	697	7	CK835498	CK835498 4059924 B
	555	42.8	4.8	709	7	CF766979	CF766979 CES000841
	556	42.8	4.8	713	7	CK831636	CK831636 4055193 B
	557	42.8	4.8	715	7	CK975545	CK975545 4106923 B
	558	42.8	4.8	730	7	CF766010	CF766010 CES007494
	559	42.8	4.8	800	7	CK774403	CK774403 963161 MA
	560	42.8	4.8	824	7	CK954605	CK954605 4094638 B
	561	42.6	4.8	310	1	AA340812	AA340812 EST46095
	562	42.6	4.8	509	4	BM536518	BM536518 ha71c01.g
	563	42.6	4.8	533	4	BM538431	BM538431 ha95e09.g
	564	42.6	4.8	536	6	CB296479	CB296479 12B22031_
	565	42.6	4.8	549	4	BM538403	BM538403 ha95c02.g
	566	42.6	4.8	582	5	BP192828	BP192828 BP192828
	567	42.6	4.8	582	5	BP210203	BP210203 BP210203
	568	42.6	4.8	582	5	BP349368	BP349368 BP349368
	569	42.6	4.8	583	5	BP210230	BP210230 BP210230
c	570	42.6	4.8	604	7	CV134188	CV134188 EST845397
	571	42.6	4.8	613	1	AI879203	AI879203 au55h01.y
	572	42.6	4.8	623	4	BM539963	BM539963 hb16d06.g
	573	42.6	4.8	636	4	BM538037	BM538037 ha89d12.g
	574	42.6	4.8	661	7	CN005962	CN005962 ip37a09.g
	575	42.6	4.8	687	4	BI679012	BI679012 SWS1055 S
	576	42.6	4.8	733	9	AG170754	AG170754 Pan trogl
	577	42.6	4.8	787	4	BG480254	BG480254 602530485
	578	42.6	4.8	815	5	BX391193	BX391193 BX391193
c	579	42.6	4.8	824	7	CV144688	CV144688 EST855897
	580	42.4	4.8	532	2	AW152789	AW152789 JALsL3C04
	581	42.2	4.7	365	7	CF507437	CF507437 USDA-FP_1
	582	42.2	4.7	406	6	CB212698	CB212698 OML02978
	583	42.2	4.7	435	7	W76454	W76454 zd61d03.r1
	584	42.2	4.7	500	7	N48390	N48390 yy43d03.r1
c	585	42.2	4.7	627	7	CF830554	CF830554 UCRCR01_0
c	586	42.2	4.7	713	7	CN191883	CN191883 UCRCS06_0
	587	42.2	4.7	728	7	CN191805	CN191805 UCRCS06_0
	588	42.2	4.7	783	7	CF830553	CF830553 UCRCR01_0
	589	42.2	4.7	896	5	BU939414	BU939414 AGENCOURT
	590	42.2	4.7	943	5	BX407903	BX407903 BX407903
c	591	42.2	4.7	947	5	BX453304	BX453304 BX453304
	592	42.2	4.7	994	5	BX325733	BX325733 BX325733
	593	42	4.7	511	7	CV135553	CV135553 EST846762
	594	42	4.7	549	5	BQ088781	BQ088781 ko36d02.y
	595	42	4.7	707	4	BI106450	BI106450 602893010
	596	41.8	4.7	289	1	AA374632	AA374632 EST86867
	597	41.8	4.7	577	6	CA304702	CA304702 As_adfo_2
	598	41.8	4.7	934	5	BX407964	BX407964 BX407964
	599	41.6	4.7	418	1	AJ282614	AJ282614 4A3A-ABA-
	600	41.6	4.7	522	9	CL964812	CL964812 OsIFCC011
	601	41.6	4.7	533	5	BX609851	BX609851 BX609851
	602	41.6	4.7	604	4	BM617525	BM617525 170006871
	603	41.6	4.7	606	7	CR536056	CR536056 CR536056
	604	41.6	4.7	641	4	BM576300	BM576300 170006871
	605	41.6	4.7	644	4	BM577753	BM577753 170006593
	606	41.6	4.7	648	2	AW162794	AW162794 au87c02.y
	607	41.6	4.7	653	7	CR536163	CR536163 CR536163
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	614	41.6	4.7	819	5	BX366874	BX366874 BX366874
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	617	41.4	4.7	222	5	BW525516	BW525516 BW525516
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	631	41	4.6	183	1	AA349303	AA349303 EST55884
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	655	41	4.6	443	6	CD686044	CD686044 EST2565 h
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	657	41	4.6	445	1	AI929098	AI929098 au65b01.y
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683	41	4.6	497	4	BM315062	BM315062 ig43a06.y
684	41	4.6	497	7	N28527	N28527 yx37b06.r1
685	41	4.6	498	1	AA459469	AA459469 aa27a07.r
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687	41	4.6	504	2	AW160972	AW160972 au77f06.y
688	41	4.6	504	4	BM845734	BM845734 K-EST0124
689	41	4.6	505	1	AI187135	AI187135 qe42g02.x
690	41	4.6	505	2	AW163389	AW163389 au94f06.y
691	41	4.6	505	6	CA771403	CA771403 io70g03.y
692	41	4.6	506	2	AW160734	AW160734 au75d06.y
693	41	4.6	506	2	AW160844	AW160844 au76d04.y
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695	41	4.6	510	7	CN267783	CN267783 170004243
696	41	4.6	514	6	CA842180	CA842180 ip29d03.y
697	41	4.6	515	4	BM263514	BM263514 ig27a09.y
698	41	4.6	515	5	BQ777251	BQ777251 il45e03.y
699	41	4.6	516	2	AW163452	AW163452 au95a02.y
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701	41	4.6	517	2	AW163490	AW163490 au95d11.y
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707	41	4.6	527	7	CN267779	CN267779 170005321
708	41	4.6	528	2	AW160648	AW160648 au67d04.y
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710	41	4.6	533	5	BM888526	BM888526 TM196 Hum
711	41	4.6	533	6	CD699921	CD699921 EST16445
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713	41	4.6	534	7	W17250	W17250 zb17d04.r1
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715	41	4.6	539	4	BM763023	BM763023 K-EST0044
716	41	4.6	542	2	AW247064	AW247064 2822606.5
717	41	4.6	542	4	BM687180	BM687180 UI-E-CQ1-
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723	41	4.6	550	6	CA397871	CA397871 cs97b10.y
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733	41	4.6	565	7	CN267797	CN267797 170005999
734	41	4.6	567	6	CA773723	CA773723 im56b08.y
735	41	4.6	568	5	BQ307679	BQ307679 MR0-BT250
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737	41	4.6	569	5	BP273427	BP273427 BP273427
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755	41	4.6	578	5	BQ417243	BQ417243 ik35e04.y
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757	41	4.6	580	5	BP212551	BP212551 BP212551
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761	41	4.6	580	5	BP260946	BP260946 BP260946
762	41	4.6	580	5	BP290375	BP290375 BP290375
763	41	4.6	580	5	BP326452	BP326452 BP326452
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765	41	4.6	580	5	BP369264	BP369264 BP369264
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774	41	4.6	581	5	BP314682	BP314682 BP314682
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776	41	4.6	581	5	BP349756	BP349756 BP349756
777	41	4.6	581	5	BU952686	BU952686 io73f08.y
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792	41	4.6	582	5	BP198378	BP198378 BP198378
793	41	4.6	582	5	BP198429	BP198429 BP198429
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796	41	4.6	582	5	BP210209	BP210209 BP210209
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813	41	4.6	582	5	BP348744	BP348744 BP348744
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	852	41	4.6	587	5	BP197166	BP197166 BP197166
	853	41	4.6	587	5	BP236120	BP236120 BP236120
	854	41	4.6	587	5	BP279410	BP279410 BP279410
	855	41	4.6	587	5	BP307384	BP307384 BP307384
	856	41	4.6	587	5	BP347271	BP347271 BP347271
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	860	41	4.6	588	5	BP318683	BP318683 BP318683
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	870	41	4.6	595	4	BI117980	BI117980 602867235
	871	41	4.6	595	5	BP382658	BP382658 BP382658
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	873	41	4.6	598	5	BP307732	BP307732 BP307732
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	875	41	4.6	599	6	CA777048	CA777048 ip02d11.y
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	879	41	4.6	603	5	BQ286358	BQ286358 ik29b05.y
	880	41	4.6	607	1	AV708805	AV708805 AV708805
	881	41	4.6	609	5	BQ307680	BQ307680 MR0-BT250
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	885	41	4.6	614	5	BU947440	BU947440 io48c05.y
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	889	41	4.6	617	5	BQ639325	BQ639325 he14b01.y
	890	41	4.6	619	5	BQ639225	BQ639225 hd32h10.y
	891	41	4.6	622	2	BE294279	BE294279 601172653
	892	41	4.6	623	4	BI669083	BI669083 603295193
	893	41	4.6	624	4	BG769486	BG769486 602742460
	894	41	4.6	626	7	CN267786	CN267786 170006000
	895	41	4.6	626	7	CN267788	CN267788 170004246
	896	41	4.6	627	1	AA166661	AA166661 zq39h02.r
	897	41	4.6	629	4	BM845129	BM845129 K-EST0123
	898	41	4.6	629	5	BQ639907	BQ639907 he21g06.y
	899	41	4.6	629	6	CA865768	CA865768 ir41d06.y
	900	41	4.6	629	6	CD675730	CD675730 fs27c04.y
	901	41	4.6	631	7	CN267792	CN267792 170006001
	902	41	4.6	632	4	BI909294	BI909294 603067254
	903	41	4.6	632	6	CB216647	CB216647 NISC_nq07
	904	41	4.6	633	5	BQ631589	BQ631589 il19e04.y
	905	41	4.6	635	5	BU078138	BU078138 im64f04.y
	906	41	4.6	637	7	CF128490	CF128490 UI-HF-ET0
	907	41	4.6	638	2	BE386167	BE386167 601277294
	908	41	4.6	638	6	CD579814	CD579814 EST_PSF00
	909	41	4.6	638	7	CK003812	CK003812 AGENCOURT
	910	41	4.6	638	7	CN267782	CN267782 170005326
	911	41	4.6	640	4	BM795311	BM795311 K-EST0077
	912	41	4.6	640	5	BU786362	BU786362 in53h08.y
	913	41	4.6	642	6	CB154997	CB154997 K-EST0213
	914	41	4.6	642	7	CK002484	CK002484 AGENCOURT
	915	41	4.6	644	4	BI459048	BI459048 603199581
	916	41	4.6	646	1	AI064998	AI064998 HA0825 Hu
	917	41	4.6	647	4	BG699607	BG699607 602679337
	918	41	4.6	648	2	BE793621	BE793621 601588637
	919	41	4.6	648	6	CA772262	CA772262 io93h08.y
	920	41	4.6	648	6	CB154425	CB154425 K-EST0212
	921	41	4.6	648	6	CD615081	CD615081 56068029J
	922	41	4.6	648	7	CN267812	CN267812 170004240
	923	41	4.6	650	1	AV708841	AV708841 AV708841
	924	41	4.6	651	1	AV702485	AV702485 AV702485
	925	41	4.6	651	1	AV713707	AV713707 AV713707
	926	41	4.6	652	7	CN267778	CN267778 170004243
	927	41	4.6	653	4	BM763989	BM763989 K-EST0045
	928	41	4.6	655	2	BE535340	BE535340 601058886
	929	41	4.6	655	4	BG703489	BG703489 602686257
	930	41	4.6	655	6	CD299152	CD299152 AGENCOURT
	931	41	4.6	657	1	AV696019	AV696019 AV696019
	932	41	4.6	660	7	CN267805	CN267805 170005831
c	933	41	4.6	661	6	CD615080	CD615080 56068029H
	934	41	4.6	662	4	BM825006	BM825006 K-EST0096
	935	41	4.6	665	7	CN267809	CN267809 170006005
	936	41	4.6	673	4	BG699276	BG699276 602678948
	937	41	4.6	673	7	CN267789	CN267789 170006001
	938	41	4.6	674	2	BE263925	BE263925 601191267
	939	41	4.6	676	2	BE281195	BE281195 601157841
	940	41	4.6	680	1	AI929714	AI929714 au63g03.y
	941	41	4.6	680	4	BF978793	BF978793 602149133
	942	41	4.6	680	4	BG680353	BG680353 602629249
	943	41	4.6	680	7	CN267802	CN267802 170006001
	944	41	4.6	684	4	BI195688	BI195688 602754237
	945	41	4.6	687	4	BM042144	BM042144 603615778
	946	41	4.6	688	2	BE732033	BE732033 601566877
	947	41	4.6	689	4	BI117838	BI117838 602866861
	948	41	4.6	689	4	BM760759	BM760759 K-EST0041
c	949	41	4.6	689	7	CK460944	CK460944 931268 MA
	950	41	4.6	691	4	BI413421	BI413421 602986784
	951	41	4.6	692	1	AV704900	AV704900 AV704900
	952	41	4.6	692	2	BE396028	BE396028 601312639
	953	41	4.6	692	7	CN267810	CN267810 170004243
	954	41	4.6	694	1	AV706232	AV706232 AV706232
	955	41	4.6	696	4	BI458231	BI458231 603199171
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	958	41	4.6	696	7	CN267804	CN267804 170005999
	959	41	4.6	697	7	CN267811	CN267811 170004240
	960	41	4.6	697	7	CO473070	CO473070 GQ0046.B3
	961	41	4.6	698	7	CN267781	CN267781 170004706
	962	41	4.6	700	4	BI666549	BI666549 603291431
	963	41	4.6	700	7	CN267813	CN267813 170004706
	964	41	4.6	702	5	BX119881	BX119881 BX119881
	965	41	4.6	703	4	BG024697	BG024697 602275635
	966	41	4.6	708	4	BI544709	BI544709 603242668
	967	41	4.6	708	6	CA775058	CA775058 ip12e09.y
	968	41	4.6	712	4	BG700005	BG700005 602681193
	969	41	4.6	712	5	BX443415	BX443415 BX443415
	970	41	4.6	713	6	CD705176	CD705176 EST21703
	971	41	4.6	714	2	BE877761	BE877761 601486328
	972	41	4.6	714	4	BG818650	BG818650 602778833
	973	41	4.6	718	2	BE260839	BE260839 601151211

974	41	4.6	718	7	CN267785	CN267785	170005999
975	41	4.6	719	1	AV703933	AV703933	AV703933
976	41	4.6	721	1	AU119336	AU119336	AU119336
977	41	4.6	722	4	BI596802	BI596802	603242888
978	41	4.6	726	6	CD580035	CD580035	EST_PSF00
979	41	4.6	728	2	BE410236	BE410236	601300047
980	41	4.6	729	2	BE297327	BE297327	601177632
981	41	4.6	730	4	BI666720	BI666720	603291941
982	41	4.6	731	7	CN267799	CN267799	170005977
983	41	4.6	733	2	BE562072	BE562072	601345882
984	41	4.6	734	4	BI822290	BI822290	603036427
985	41	4.6	734	4	BI857454	BI857454	603384423
986	41	4.6	735	4	BG758256	BG758256	602712437
987	41	4.6	736	1	AV690380	AV690380	AV690380
988	41	4.6	736	4	BM046111	BM046111	603625827
989	41	4.6	737	6	CB986092	CB986092	AGENCOURT
990	41	4.6	741	4	BG756445	BG756445	602715777
991	41	4.6	742	2	BF130104	BF130104	601817994
992	41	4.6	745	1	AU117759	AU117759	AU117759
993	41	4.6	745	6	CA776088	CA776088	io99e07.y
c 994	41	4.6	746	4	BI084883	BI084883	602869450
995	41	4.6	747	4	BG481383	BG481383	602528738
996	41	4.6	747	4	BG701259	BG701259	602682930
997	41	4.6	747	4	BG702672	BG702672	602684211
998	41	4.6	747	4	BI860435	BI860435	603385086
999	41	4.6	749	4	BG329629	BG329629	602429234
1000	41	4.6	749	4	BI598448	BI598448	603246959
1001	41	4.6	750	4	BF967466	BF967466	602287396
1002	41	4.6	750	4	BI838210	BI838210	603083128
1003	41	4.6	752	4	BG706096	BG706096	602669054
1004	41	4.6	752	4	BI834340	BI834340	603084371
1005	41	4.6	753	4	BG706943	BG706943	602672132
1006	41	4.6	754	1	AU129706	AU129706	AU129706
1007	41	4.6	756	4	BG709157	BG709157	602675033
1008	41	4.6	758	4	BF965549	BF965549	602277015
1009	41	4.6	760	1	AU120318	AU120318	AU120318
1010	41	4.6	761	1	AV707449	AV707449	AV707449
1011	41	4.6	762	4	BI458683	BI458683	603199817
1012	41	4.6	762	4	BI871433	BI871433	603394575
1013	41	4.6	763	4	BI916228	BI916228	603178126
1014	41	4.6	763	6	CD245504	CD245504	AGENCOURT
1015	41	4.6	763	7	CK460242	CK460242	930500 MA
1016	41	4.6	765	4	BI458324	BI458324	603199281
1017	41	4.6	765	4	BM043594	BM043594	603620045
1018	41	4.6	766	4	BG545865	BG545865	602573150
1019	41	4.6	768	4	BG471148	BG471148	602512231
1020	41	4.6	771	2	BE257010	BE257010	601117413
1021	41	4.6	772	4	BI859899	BI859899	603386029
1022	41	4.6	774	4	BG701839	BG701839	602683182
1023	41	4.6	774	4	BI457707	BI457707	603198144
1024	41	4.6	774	4	BI669450	BI669450	603294144
1025	41	4.6	774	5	BU602488	BU602488	AGENCOURT
1026	41	4.6	775	5	BP456349	BP456349	BP456349
1027	41	4.6	777	4	BG707505	BG707505	602670743
1028	41	4.6	778	4	BI256490	BI256490	602977841
1029	41	4.6	779	4	BI488961	BI488961	603021684
1030	41	4.6	779	7	CN267784	CN267784	170006001
1031	41	4.6	780	4	BG497308	BG497308	602537874
1032	41	4.6	780	4	BG777405	BG777405	602664687
1033	41	4.6	780	4	BI602437	BI602437	603252223
1034	41	4.6	781	4	BI548098	BI548098	603189419
c1035	41	4.6	782	6	CA774799	CA774799	ip12e09.x
1036	41	4.6	783	5	BQ678207	BQ678207	AGENCOURT
1037	41	4.6	784	4	BG770696	BG770696	602734041
1038	41	4.6	784	7	CF126406	CF126406	UI-HF-ET0
1039	41	4.6	786	4	BG427360	BG427360	602494451
1040	41	4.6	787	4	BG723355	BG723355	602694010
c1041	41	4.6	787	6	CA775867	CA775867	io99e07.x
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1043	41	4.6	791	4	BG105154	BG105154	602313077
1044	41	4.6	792	4	BG748643	BG748643	602706345
1045	41	4.6	793	2	BE259402	BE259402	601106595
1046	41	4.6	794	4	BI834911	BI834911	603090179
1047	41	4.6	797	2	BF342370	BF342370	602013163
1048	41	4.6	797	2	BE733146	BE733146	601567427
1049	41	4.6	798	4	BM013911	BM013911	603639527
c1050	41	4.6	801	6	CA774599	CA774599	ip25c12.x
1051	41	4.6	802	4	BG714428	BG714428	602669957
1052	41	4.6	802	4	BG715293	BG715293	602676180
1053	41	4.6	806	4	BI598116	BI598116	603252357
1054	41	4.6	808	4	BG706219	BG706219	602669504
1055	41	4.6	809	4	BG714671	BG714671	602677025
1056	41	4.6	812	4	BG709015	BG709015	602675164
1057	41	4.6	812	4	BI084088	BI084088	602869450
1058	41	4.6	812	5	BU857781	BU857781	AGENCOURT
1059	41	4.6	816	5	BX429127	BX429127	BX429127
1060	41	4.6	816	6	CD579352	CD579352	EST_PSF00
1061	41	4.6	817	4	BG766486	BG766486	602739247
1062	41	4.6	818	4	BG334977	BG334977	602403411
1063	41	4.6	818	4	BI772744	BI772744	603053290
1064	41	4.6	819	4	BI548646	BI548646	603196809
1065	41	4.6	821	2	BF338033	BF338033	602035919
1066	41	4.6	821	4	BG818754	BG818754	602779080
1067	41	4.6	821	4	BI836372	BI836372	603083078
1068	41	4.6	822	5	BU957273	BU957273	AGENCOURT
1069	41	4.6	823	4	BI113718	BI113718	602860912
1070	41	4.6	823	4	BI551290	BI551290	603194695
1071	41	4.6	824	4	BI089078	BI089078	602853446
1072	41	4.6	828	5	BU858045	BU858045	AGENCOURT
1073	41	4.6	829	4	BG480070	BG480070	602530164
1074	41	4.6	830	4	BI818474	BI818474	603032763
1075	41	4.6	831	4	BG386159	BG386159	602455341
1076	41	4.6	831	4	BI552625	BI552625	603197963
1077	41	4.6	832	4	BG170349	BG170349	602323248
1078	41	4.6	834	4	BG763051	BG763051	602734930
1079	41	4.6	835	4	BI258624	BI258624	602969559
1080	41	4.6	835	6	CD580198	CD580198	EST_PSF00
1081	41	4.6	836	5	BU521565	BU521565	AGENCOURT
1082	41	4.6	840	4	BI548106	BI548106	603189440
1083	41	4.6	841	4	BG536935	BG536935	602564679
1084	41	4.6	841	4	BG696068	BG696068	602658028
1085	41	4.6	841	4	BI089561	BI089561	602854426
1086	41	4.6	846	4	BG024729	BG024729	602275674
1087	41	4.6	846	4	BI458064	BI458064	603199076
1088	41	4.6	846	4	BI599071	BI599071	603250472
1089	41	4.6	847	2	BE799439	BE799439	601589466
1090	41	4.6	847	5	BX384604	BX384604	BX384604
1091	41	4.6	850	4	BG252637	BG252637	602366275
1092	41	4.6	850	4	BI823692	BI823692	603040808
1093	41	4.6	851	4	BG702622	BG702622	602684337
1094	41	4.6	852	2	BE613926	BE613926	601504046
1095	41	4.6	852	4	BG683023	BG683023	602651382
1096	41	4.6	854	5	BX339855	BX339855	BX339855
1097	41	4.6	856	5	BX371269	BX371269	BX371269
1098	41	4.6	857	2	BF685690	BF685690	602140561
1099	41	4.6	857	4	BG474671	BG474671	602517623
1100	41	4.6	860	2	BF305939	BF305939	601889230
1101	41	4.6	860	4	BG706041	BG706041	602669184
1102	41	4.6	860	5	BX453306	BX453306	BX453306
1103	41	4.6	861	5	BQ670136	BQ670136	AGENCOURT
1104	41	4.6	862	2	BF688570	BF688570	602184887
1105	41	4.6	863	2	BE867854	BE867854	601443627
1106	41	4.6	864	4	BM452032	BM452032	AGENCOURT
1107	41	4.6	864	5	BQ227746	BQ227746	AGENCOURT
1108	41	4.6	865	6	CD107250	CD107250	AGENCOURT
1109	41	4.6	868	2	BE884616	BE884616	601506620
1110	41	4.6	868	5	BU189215	BU189215	AGENCOURT
1111	41	4.6	868	5	BX393556	BX393556	BX393556
1112	41	4.6	868	5	BX410793	BX410793	BX410793
1113	41	4.6	870	4	BG740268	BG740268	602630687
1114	41	4.6	871	6	CA488158	CA488158	AGENCOURT
1115	41	4.6	872	4	BG760549	BG760549	602716989
1116	41	4.6	873	4	BG696626	BG696626	602658925
1117	41	4.6	873	4	BI666628	BI666628	603291333
1118	41	4.6	874	4	BG432846	BG432846	602496054
1119	41	4.6	874	4	BG772976	BG772976	602721231

1120	41	4.6	875	5	BX378103	BX378103	BX378103
1121	41	4.6	875	6	CD246326	CD246326	AGENCOURT
1122	41	4.6	876	2	BF314060	BF314060	601902313
1123	41	4.6	879	4	BG701129	BG701129	602681975
1124	41	4.6	880	4	BG715709	BG715709	602676986
1125	41	4.6	880	5	BU155894	BU155894	AGENCOURT
1126	41	4.6	880	5	BX371308	BX371308	BX371308
1127	41	4.6	880	6	CD516072	CD516072	AGENCOURT
1128	41	4.6	881	4	BI861349	BI861349	603386549
1129	41	4.6	881	5	BQ423981	BQ423981	AGENCOURT
1130	41	4.6	881	5	BQ649174	BQ649174	AGENCOURT
1131	41	4.6	883	2	BF034634	BF034634	601455066
1132	41	4.6	885	5	BQ950022	BQ950022	AGENCOURT
1133	41	4.6	888	5	BQ690722	BQ690722	AGENCOURT
1134	41	4.6	888	5	BQ921435	BQ921435	AGENCOURT
1135	41	4.6	888	5	BU192617	BU192617	AGENCOURT
1136	41	4.6	889	5	BX407971	BX407971	BX407971
1137	41	4.6	890	5	BU155276	BU155276	AGENCOURT
1138	41	4.6	891	5	BX407976	BX407976	BX407976
1139	41	4.6	892	4	BG336009	BG336009	602404762
1140	41	4.6	894	5	BQ690812	BQ690812	AGENCOURT
1141	41	4.6	894	5	BU930889	BU930889	AGENCOURT
1142	41	4.6	895	5	BQ648664	BQ648664	AGENCOURT
1143	41	4.6	896	5	BQ879197	BQ879197	AGENCOURT
1144	41	4.6	896	5	BX410377	BX410377	BX410377
1145	41	4.6	897	4	BI762223	BI762223	603049133
1146	41	4.6	897	5	BQ653009	BQ653009	AGENCOURT
1147	41	4.6	897	5	BU177802	BU177802	AGENCOURT
1148	41	4.6	899	6	CD579440	CD579440	EST_PSF00
1149	41	4.6	901	4	BG536429	BG536429	602564527
1150	41	4.6	901	5	BQ883577	BQ883577	AGENCOURT
1151	41	4.6	901	5	BQ942934	BQ942934	AGENCOURT
1152	41	4.6	903	5	BQ212241	BQ212241	AGENCOURT
1153	41	4.6	904	4	BG429778	BG429778	602493789
1154	41	4.6	904	5	BU956399	BU956399	AGENCOURT
1155	41	4.6	906	5	BU526814	BU526814	AGENCOURT
1156	41	4.6	907	5	BX341929	BX341929	BX341929
1157	41	4.6	907	5	BX449922	BX449922	BX449922
1158	41	4.6	908	5	BU957534	BU957534	AGENCOURT
1159	41	4.6	909	5	BU190128	BU190128	AGENCOURT
1160	41	4.6	911	3	CR608267	CR608267	full-leng
1161	41	4.6	912	4	BI602026	BI602026	603244321
1162	41	4.6	914	5	BU956406	BU956406	AGENCOURT
1163	41	4.6	915	5	BQ918779	BQ918779	AGENCOURT
1164	41	4.6	916	4	BG254893	BG254893	602369337
1165	41	4.6	918	2	BE880533	BE880533	601490926
1166	41	4.6	919	2	BF128578	BF128578	601810829
1167	41	4.6	919	5	BQ649016	BQ649016	AGENCOURT
1168	41	4.6	919	5	BU849974	BU849974	AGENCOURT
1169	41	4.6	920	5	BX367637	BX367637	BX367637
c1170	41	4.6	920	5	BX371268	BX371268	BX371268
1171	41	4.6	922	4	BM452020	BM452020	AGENCOURT
1172	41	4.6	923	2	BF310992	BF310992	601898306
1173	41	4.6	924	5	BU181764	BU181764	AGENCOURT
1174	41	4.6	926	4	BG249593	BG249593	602319685
1175	41	4.6	926	5	BQ678799	BQ678799	AGENCOURT
1176	41	4.6	927	4	BI597726	BI597726	603248381
1177	41	4.6	927	5	BX381359	BX381359	BX381359
1178	41	4.6	928	5	BX419665	BX419665	BX419665
1179	41	4.6	929	5	BU902842	BU902842	AGENCOURT
1180	41	4.6	929	5	BX407956	BX407956	BX407956
1181	41	4.6	930	4	BI917404	BI917404	603184946
1182	41	4.6	931	5	BX407967	BX407967	BX407967
1183	41	4.6	933	2	BF316293	BF316293	601901841
1184	41	4.6	933	4	BG765411	BG765411	602738879
1185	41	4.6	933	5	BU944599	BU944599	AGENCOURT
1186	41	4.6	933	5	BX325766	BX325766	BX325766
1187	41	4.6	934	5	BQ650976	BQ650976	AGENCOURT
1188	41	4.6	935	5	BX423325	BX423325	BX423325
1189	41	4.6	936	2	BF344500	BF344500	602014906
1190	41	4.6	936	2	BF686565	BF686565	602143479
1191	41	4.6	936	5	BQ720893	BQ720893	AGENCOURT
1192	41	4.6	936	5	BX407830	BX407830	BX407830
1193	41	4.6	937	2	BE548004	BE548004	601072029
1194	41	4.6	937	5	BU846284	BU846284	AGENCOURT
1195	41	4.6	938	4	BG706215	BG706215	602669496
1196	41	4.6	939	2	BE733895	BE733895	601568363
1197	41	4.6	939	4	BG253274	BG253274	602365747
1198	41	4.6	939	4	BI835668	BI835668	603087641
1199	41	4.6	940	5	BQ883899	BQ883899	AGENCOURT
1200	41	4.6	940	5	BQ948050	BQ948050	AGENCOURT
1201	41	4.6	941	5	BQ672954	BQ672954	AGENCOURT
1202	41	4.6	942	4	BG112714	BG112714	602282275
1203	41	4.6	945	2	BE731272	BE731272	601567172
1204	41	4.6	945	4	BG769616	BG769616	602744528
1205	41	4.6	946	5	BQ681865	BQ681865	AGENCOURT
1206	41	4.6	947	4	BF972336	BF972336	602240641
1207	41	4.6	947	5	BQ675611	BQ675611	AGENCOURT
c1208	41	4.6	947	5	BX362889	BX362889	BX362889
1209	41	4.6	948	5	BQ677444	BQ677444	AGENCOURT
1210	41	4.6	949	5	BX367611	BX367611	BX367611
1211	41	4.6	950	5	BQ943875	BQ943875	AGENCOURT
1212	41	4.6	952	4	BI458280	BI458280	603199230
1213	41	4.6	952	5	BQ648518	BQ648518	AGENCOURT
1214	41	4.6	953	5	BU955758	BU955758	AGENCOURT
1215	41	4.6	954	5	BU556653	BU556653	AGENCOURT
1216	41	4.6	957	5	BQ672035	BQ672035	AGENCOURT
1217	41	4.6	957	5	BU508821	BU508821	AGENCOURT
1218	41	4.6	958	4	BF983939	BF983939	602304512
1219	41	4.6	958	6	CD579239	CD579239	EST_PSF00
1220	41	4.6	959	2	BF312303	BF312303	601898827
1221	41	4.6	960	4	BG254668	BG254668	602368642
1222	41	4.6	960	5	BX421025	BX421025	BX421025
1223	41	4.6	961	4	BI091223	BI091223	602856068
1224	41	4.6	961	5	BX346775	BX346775	BX346775
1225	41	4.6	962	4	BF976370	BF976370	602244311
1226	41	4.6	962	4	BI458107	BI458107	603198527
1227	41	4.6	963	4	BF973496	BF973496	602242828
1228	41	4.6	965	5	BQ684559	BQ684559	AGENCOURT
1229	41	4.6	966	5	BU552849	BU552849	AGENCOURT
1230	41	4.6	966	5	BU856890	BU856890	AGENCOURT
1231	41	4.6	967	5	BU179259	BU179259	AGENCOURT
1232	41	4.6	970	5	BQ647918	BQ647918	AGENCOURT
1233	41	4.6	972	4	BI838336	BI838336	603083277
1234	41	4.6	972	5	BX346733	BX346733	BX346733
1235	41	4.6	972	5	BX362082	BX362082	BX362082
1236	41	4.6	973	5	BQ677943	BQ677943	AGENCOURT
1237	41	4.6	974	5	BQ927896	BQ927896	AGENCOURT
1238	41	4.6	976	4	BI458424	BI458424	603198805
1239	41	4.6	978	4	BG762136	BG762136	602717723
1240	41	4.6	978	4	BG829113	BG829113	602752463
1241	41	4.6	982	4	BG695994	BG695994	602658138
1242	41	4.6	982	5	BX428113	BX428113	BX428113
1243	41	4.6	984	5	BQ680261	BQ680261	AGENCOURT
1244	41	4.6	986	5	BX453305	BX453305	BX453305
c1245	41	4.6	987	5	BX464203	BX464203	BX464203
1246	41	4.6	988	5	BQ050179	BQ050179	AGENCOURT
1247	41	4.6	988	5	BX440961	BX440961	BX440961
1248	41	4.6	989	5	BX367651	BX367651	BX367651
1249	41	4.6	989	5	BX378324	BX378324	BX378324
1250	41	4.6	990	6	CD514922	CD514922	AGENCOURT
1251	41	4.6	991	5	BX354037	BX354037	BX354037
1252	41	4.6	991	5	BX429006	BX429006	BX429006
c1253	41	4.6	991	5	BX443911	BX443911	BX443911
1254	41	4.6	992	4	BG678514	BG678514	602626186
1255	41	4.6	992	5	BX407683	BX407683	BX407683
1256	41	4.6	993	5	BQ668625	BQ668625	AGENCOURT
1257	41	4.6	993	5	BX349732	BX349732	BX349732
1258	41	4.6	993	5	BX407732	BX407732	BX407732
1259	41	4.6	995	5	BQ649083	BQ649083	AGENCOURT
1260	41	4.6	996	5	BX362890	BX362890	BX362890
1261	41	4.6	1002	3	CR615482	CR615482	full-leng
1262	41	4.6	1003	5	BX440743	BX440743	BX440743
1263	41	4.6	1005	4	BM472348	BM472348	AGENCOURT
1264	41	4.6	1008	5	BX440682	BX440682	BX440682
1265	41	4.6	1010	5	BX325728	BX325728	BX325728

1266	41	4.6	1014	5	BX381871	BX381871	BX381871
1267	41	4.6	1016	5	BX388454	BX388454	BX388454
1268	41	4.6	1017	5	BX432905	BX432905	BX432905
1269	41	4.6	1017	5	BX463478	BX463478	BX463478
1270	41	4.6	1023	5	BX443912	BX443912	BX443912
1271	41	4.6	1025	2	BE900878	BE900878	601673879
1272	41	4.6	1026	4	BM468290	BM468290	AGENCOURT
1273	41	4.6	1026	5	BX371312	BX371312	BX371312
1274	41	4.6	1026	5	BX407834	BX407834	BX407834
1275	41	4.6	1027	5	BM922145	BM922145	AGENCOURT
1276	41	4.6	1029	5	BX437989	BX437989	BX437989
1277	41	4.6	1031	3	CR596355	CR596355	full-leng
1278	41	4.6	1031	5	BQ072218	BQ072218	AGENCOURT
1279	41	4.6	1032	4	BM451389	BM451389	AGENCOURT
1280	41	4.6	1032	5	BX423158	BX423158	BX423158
1281	41	4.6	1032	5	BX444343	BX444343	BX444343
1282	41	4.6	1032	5	BX444617	BX444617	BX444617
1283	41	4.6	1034	5	BX463439	BX463439	BX463439
1284	41	4.6	1035	3	CR594432	CR594432	full-leng
1285	41	4.6	1036	4	BI599223	BI599223	603250253
1286	41	4.6	1036	4	BM563063	BM563063	AGENCOURT
1287	41	4.6	1036	5	BQ063183	BQ063183	AGENCOURT
1288	41	4.6	1036	5	BX399444	BX399444	BX399444
1289	41	4.6	1036	5	BX422909	BX422909	BX422909
1290	41	4.6	1037	5	BQ681956	BQ681956	AGENCOURT
1291	41	4.6	1037	5	BX464204	BX464204	BX464204
1292	41	4.6	1038	4	BM463607	BM463607	AGENCOURT
1293	41	4.6	1038	5	BM918100	BM918100	AGENCOURT
1294	41	4.6	1038	5	BX343014	BX343014	BX343014
1295	41	4.6	1040	3	BC018799	BC018799	Homo sapi
1296	41	4.6	1040	5	BX458778	BX458778	BX458778
1297	41	4.6	1043	3	CR618909	CR618909	full-leng
1298	41	4.6	1045	3	CR590878	CR590878	full-leng
1299	41	4.6	1047	5	BX461606	BX461606	BX461606
1300	41	4.6	1048	5	BM903594	BM903594	AGENCOURT
1301	41	4.6	1050	4	BG767863	BG767863	602741363
1302	41	4.6	1051	4	BI599116	BI599116	603246331
1303	41	4.6	1064	5	BX457584	BX457584	BX457584
1304	41	4.6	1066	4	BM450293	BM450293	AGENCOURT
1305	41	4.6	1068	5	BM916361	BM916361	AGENCOURT
1306	41	4.6	1073	4	BM562453	BM562453	AGENCOURT
1307	41	4.6	1073	5	BQ072062	BQ072062	AGENCOURT
1308	41	4.6	1079	2	BF684932	BF684932	602142067
1309	41	4.6	1082	3	CR595335	CR595335	full-leng
1310	41	4.6	1091	5	BU162554	BU162554	AGENCOURT
1311	41	4.6	1101	5	BQ421305	BQ421305	AGENCOURT
1312	41	4.6	1105	5	BQ071464	BQ071464	AGENCOURT
1313	41	4.6	1112	4	BM046629	BM046629	603626722
1314	41	4.6	1122	5	BM918663	BM918663	AGENCOURT
1315	41	4.6	1128	4	BM453466	BM453466	AGENCOURT
1316	41	4.6	1141	2	BF686267	BF686267	602142728
1317	41	4.6	1143	5	BQ071466	BQ071466	AGENCOURT
1318	41	4.6	1148	4	BG394135	BG394135	602456312
1319	41	4.6	1148	5	BU839415	BU839415	AGENCOURT
1320	41	4.6	1159	5	BM922596	BM922596	AGENCOURT
1321	41	4.6	1178	4	BM465427	BM465427	AGENCOURT
1322	41	4.6	1179	5	BU902043	BU902043	AGENCOURT
1323	41	4.6	1190	5	BM926597	BM926597	AGENCOURT
1324	41	4.6	1216	5	BU517104	BU517104	AGENCOURT
1325	41	4.6	1258	4	BM809552	BM809552	AGENCOURT
1326	41	4.6	1320	5	BQ067654	BQ067654	AGENCOURT
1327	41	4.6	1332	3	CR621357	CR621357	full-leng
1328	41	4.6	1355	3	CR612913	CR612913	full-leng
1329	41	4.6	1413	3	CR595492	CR595492	full-leng
1330	41	4.6	1422	3	CR626465	CR626465	full-leng
1331	41	4.6	1440	3	CR598446	CR598446	full-leng
1332	41	4.6	1579	5	BM921938	BM921938	AGENCOURT
1333	40.8	4.6	310	2	AW870860	AW870860	ra51f05.y
1334	40.8	4.6	517	7	CF830497	CF830497	UCRCR01_0
1335	40.8	4.6	630	1	AU003812	AU003812	AU003812
1336	40.8	4.6	652	1	AU003778	AU003778	AU003778
1337	40.8	4.6	698	7	CK939149	CK939149	CGF100443
1338	40.8	4.6	719	7	CF829560	CF829560	UCRCR01_0
1339	40.8	4.6	733	7	CF829562	CF829562	UCRCR01_0
1340	40.8	4.6	751	7	CF829520	CF829520	UCRCR01_0
1341	40.8	4.6	754	1	AU003770	AU003770	AU003770
1342	40.8	4.6	762	7	CK938225	CK938225	CGF100447
c1343	40.8	4.6	837	7	CF829561	CF829561	UCRCR01_0
c1344	40.8	4.6	846	7	CF829559	CF829559	UCRCR01_0
c1345	40.8	4.6	849	7	CF829519	CF829519	UCRCR01_0
c1346	40.8	4.6	911	7	CF829947	CF829947	UCRCR01_0
1347	40.6	4.6	393	4	BI457492	BI457492	603185865
1348	40.6	4.6	491	2	BF483056	BF483056	WHE2314_C
1349	40.6	4.6	494	6	CD884363	CD884363	F1.116G19
1350	40.6	4.6	505	2	BE498304	BE498304	WHE0963_B
1351	40.6	4.6	532	4	BM343659	BM343659	rr41d02.y
1352	40.6	4.6	551	2	BE590867	BE590867	WHE0855_C
1353	40.6	4.6	575	6	CD884008	CD884008	F1.115C14
1354	40.6	4.6	597	6	CD883599	CD883599	F1.113N14
1355	40.6	4.6	603	4	BM354566	BM354566	rr06b03.y
1356	40.6	4.6	605	1	AU005893	AU005893	AU005893
1357	40.6	4.6	606	4	BM344987	BM344987	rr62b03.y
1358	40.6	4.6	618	4	BM343451	BM343451	rr38g01.y
1359	40.6	4.6	622	4	BM344884	BM344884	rr60f02.y
1360	40.6	4.6	626	6	CD881060	CD881060	F1.100N03
1361	40.6	4.6	636	6	CD884599	CD884599	F1.117C12
1362	40.6	4.6	689	6	CD882410	CD882410	F1.106J20
1363	40.6	4.6	695	6	CD861747	CD861747	AZO1.003J
1364	40.6	4.6	712	7	CK937369	CK937369	CGF100451
1365	40.6	4.6	762	7	CV200558	CV200558	km05e10.y
1366	40.6	4.6	896	5	BX346779	BX346779	BX346779
c1367	40.4	4.5	503	7	CV134317	CV134317	EST845526
c1368	40.4	4.5	742	7	CN783493	CN783493	EST782184
1369	40	4.5	271	1	AA384661	AA384661	EST98230
1370	40	4.5	450	5	BX393014	BX393014	BX393014
c1371	40	4.5	460	9	CE054150	CE054150	tigr-gss-
1372	40	4.5	473	1	AA307219	AA307219	EST178179
1373	40	4.5	522	2	AW981994	AW981994	PC22E11 P
1374	40	4.5	531	5	BX616134	BX616134	BX616134
1375	40	4.5	573	6	CB095487	CB095487	ie90a11.b
1376	40	4.5	679	7	CF476310	CF476310	RTWW2_22_
1377	40	4.5	704	7	CN044875	CN044875	v11_p53_g
1378	40	4.5	721	7	CN043052	CN043052	v11_p45_c
1379	40	4.5	729	1	AJ803471	AJ803471	AJ803471
1380	40	4.5	729	9	CE774531	CE774531	tigr-gss-
c1381	40	4.5	771	6	CA774566	CA774566	ip24h03.x
1382	40	4.5	790	9	CE565244	CE565244	tigr-gss-
c1383	40	4.5	804	5	BM981575	BM981575	UI-CF-EN1
c1384	40	4.5	806	6	CA771982	CA771982	io93h08.x
1385	40	4.5	988	5	BX380693	BX380693	BX380693
1386	39.8	4.5	611	7	CK564101	CK564101	rswpb0_00
c1387	39.8	4.5	629	5	BW593661	BW593661	BW593661
1388	39.8	4.5	657	7	CF803751	CF803751	rg75a04.y
1389	39.8	4.5	678	7	CF979538	CF979538	rg78a07.y
1390	39.8	4.5	716	7	CF804064	CF804064	rg67g08.y
1391	39.8	4.5	897	7	CK935601	CK935601	CGF100455
1392	39.6	4.4	274	1	AA318079	AA318079	EST20104
1393	39.6	4.4	349	7	CO261239	CO261239	4133367 B
1394	39.6	4.4	350	5	BY009435	BY009435	BY009435
1395	39.6	4.4	488	7	CK495153	CK495153	rswbb0_00
1396	39.6	4.4	523	7	CK496088	CK496088	rswbb0_00
1397	39.6	4.4	557	7	CK499844	CK499844	rswbb0_01
1398	39.6	4.4	561	5	BP277453	BP277453	BP277453
1399	39.6	4.4	567	7	CK517810	CK517810	rswjb0_00
1400	39.6	4.4	584	5	BP305122	BP305122	BP305122
1401	39.6	4.4	584	7	CK488177	CK488177	rswab0_00
1402	39.6	4.4	586	7	CK490785	CK490785	rswab0_00
1403	39.6	4.4	634	7	CK562966	CK562966	rswpb0_00
1404	39.6	4.4	639	7	CK486706	CK486706	rswab0_00
1405	39.6	4.4	834	7	CK938391	CK938391	CGF100444
1406	39.4	4.4	302	6	CB700604	CB700604	AMGNNUC:N
1407	39.4	4.4	419	6	CB107087	CB107087	K-EST0145
1408	39.4	4.4	427	7	CO645472	CO645472	ILLUMIGEN
1409	39.4	4.4	427	7	CO645628	CO645628	ILLUMIGEN
1410	39.4	4.4	427	7	CO646240	CO646240	ILLUMIGEN
1411	39.4	4.4	445	2	AW161247	AW161247	au70d04.y

1412	39.4	4.4	458	1	AI815622	AI815622 au43c05.y
1413	39.4	4.4	562	5	BU605319	BU605319 mah89g07.
1414	39.4	4.4	563	7	CF982102	CF982102 maj77f12.
1415	39.4	4.4	564	4	BM641012	BM641012 170006873
1416	39.4	4.4	581	5	BP308553	BP308553
1417	39.4	4.4	582	5	BP347278	BP347278 BP347278
1418	39.4	4.4	583	5	BP321886	BP321886 BP321886
1419	39.4	4.4	618	5	BP382310	BP382310 BP382310
1420	39.4	4.4	622	5	BP381919	BP381919 BP381919
1421	39.4	4.4	638	4	BI545447	BI545447 603187601
1422	39.4	4.4	650	4	BG714233	BG714233 602674912
1423	39.4	4.4	654	4	BM606356	BM606356 170006870
1424	39.4	4.4	669	7	CO644619	CO644619 ILLUMIGEN
1425	39.4	4.4	669	7	CO646125	CO646125 ILLUMIGEN
1426	39.4	4.4	686	7	CO582521	CO582521 ILLUMIGEN
1427	39.4	4.4	728	6	CB553238	CB553238 MMSP0059_
1428	39.4	4.4	739	4	BI668405	BI668405 603292679
1429	39.4	4.4	760	7	CF127685	CF127685 UI-HF-ET0
1430	39.4	4.4	766	1	AL933213	AL933213 AL933213
1431	39.4	4.4	837	2	BE867323	BE867323 601442401
1432	39.4	4.4	842	4	BG036691	BG036691 602286418
1433	39.4	4.4	878	4	BI553720	BI553720 603190657
1434	39.4	4.4	911	4	BM461855	BM461855 AGENCOURT
1435	39.4	4.4	916	4	BG248680	BG248680 602400858
1436	39.4	4.4	922	4	BI552709	BI552709 603193960
1437	39.4	4.4	934	5	BQ276743	BQ276743 AGENCOURT
1438	39.4	4.4	945	5	BQ423945	BQ423945 AGENCOURT
1439	39.4	4.4	988	7	CN803108	CN803108 ILLUMIGEN
1440	39.2	4.4	280	9	CG486821	CG486821 OST22015
1441	39.2	4.4	378	6	CA395207	CA395207 cs61f01.y
1442	39.2	4.4	509	7	CR754114	CR754114 CR754114
1443	39	4.4	318	5	BX609821	BX609821 BX609821
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1445	39	4.4	345	1	AA684739	AA684739 EST105252
1446	39	4.4	372	7	CO265028	EK141262.
1447	39	4.4	441	7	CO332000	CO332000 EK302260.
1448	39	4.4	577	4	BI626077	BI626077 RH66610.5
1449	39	4.4	580	2	BE206935	BE206935 ba06e05.y
1450	39	4.4	600	6	CA169382	CA169382 SCJFSB101
1451	39	4.4	632	4	BI589276	BI589276 RH31664.5
1452	39	4.4	661	6	CA147028	CA147028 SCCCRZ100
1453	39	4.4	664	5	BQ605265	BQ605265 ar02-g03
1454	39	4.4	665	1	AI239220	AI239220 GM08640.5
1455	39	4.4	671	4	BI607231	BI607231 RH74250.5
1456	39	4.4	673	5	BP383345	BP383345 BP383345
1457	39	4.4	792	1	AI405423	AI405423 GH25425.5
c1458	39	4.4	812	2	AW940975	AW940975 GH25425.3
1459	38.8	4.4	385	5	BY105455	BY105455 BY105455
1460	38.8	4.4	578	5	BP259841	BP259841 BP259841
c1461	38.6	4.3	284	7	CO870920	rt65b03.y
1462	38.6	4.3	305	1	AV045990	AV045990 AV045990
1463	38.6	4.3	465	6	CB715370	CB715370 AMGNNUC:M
c1464	38.6	4.3	691	9	AG596854	AG596854 Mus muscu
1465	38.6	4.3	718	9	AG000222	AG000222 Homo sapi
c1466	38.6	4.3	1101	9	CNS017SY	AL108460 Drosophil
1467	38.4	4.3	350	4	BM600638	BM600638 170006870
1468	38.4	4.3	350	7	N86577	N86577 J8918F Huma
1469	38.4	4.3	354	1	AA686902	AA686902 EST111665
1470	38.4	4.3	365	7	CF791921	CF791921 880285 MA
1471	38.4	4.3	403	5	BW196302	BW196302 BW196302
1472	38.4	4.3	446	1	AA286635	AA286635 vb75b09.r
1473	38.4	4.3	471	7	CN685909	E0216G02-
1474	38.4	4.3	635	2	AW107102	AW107102 um18g05.y
1475	38.4	4.3	689	5	BX916481	BX916481 BX916481
1476	38.4	4.3	787	2	BF303509	BF303509 602030048
1477	38.4	4.3	807	4	BG709320	BG709320 602673340
1478	38.4	4.3	886	6	CA467194	CA467194 AGENCOURT
c1479	38.4	4.3	980	5	BX407833	BX407833 BX407833
c1480	38.2	4.3	258	7	CR471768	CR471768 CR471768
1481	38.2	4.3	475	6	CB728858	CB728858 AMGNNUC:N
1482	38.2	4.3	479	6	CB731074	CB731074 AMGNNUC:N
c1483	38.2	4.3	509	7	CR755384	CR755384 CR755384
1484	38.2	4.3	572	7	CF803753	CF803753 rg75a06.y
1485	38.2	4.3	591	7	CF803816	CF803816 rg75g08.y
1486	38.2	4.3	653	7	CF803807	CF803807 rg75f11.y
1487	38.2	4.3	662	7	CF803800	CF803800 rg75f03.y
1488	38.2	4.3	668	4	BM790151	BM790151 K-EST0069
1489	38.2	4.3	670	7	CF803684	CF803684 rg74b12.y
1490	38.2	4.3	708	4	BI275916	BI275916 UI-R-CX0-
1491	38.2	4.3	911	6	CB315099	CB315099 AGENCOURT
1492	38	4.3	308	1	AA326196	AA326196 EST29344
1493	38	4.3	540	7	CK537696	CK537696 rswgb0_00
1494	38	4.3	597	4	BI387272	BI387272 BFL26_001
1495	38	4.3	600	2	AW327467	AW327467 dq03g04.x
1496	38	4.3	651	7	CK537474	CK537474 rswgb0_00
1497	38	4.3	756	4	BI200187	BI200187 602763692
1498	38	4.3	793	7	CN823815	CN823815 Oa_splbn_
1499	38	4.3	840	7	CN822461	CN822461 Oa_splbn_
1500	38	4.3	1033	5	BX443047	BX443047 BX443047

ALIGNMENTS

RESULT 1
AY037148
LOCUS AY037148 874 bp mRNA linear HTC 02-JUL-2001
DEFINITION Homo sapiens phosphatidylethanolamine binding protein mRNA, complete cds.
ACCESSION AY037148
VERSION AY037148.1 GI:14585854
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS Zhang,W., Li,N., Wan,T. and Cao,X.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2001) Department of Immunology, Second Military Medical University, 800 Xiangyin Rd., Shanghai 200433, P.R.China
FEATURES Location/Qualifiers
source 1. .874
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
CDS 66. .749
/codon_start=1
/product="phosphatidylethanolamine binding protein"
/protein_id="AAK67629.1"
/db_xref="GI:14585855"
/translation="MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQ
GLEVFYPELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSR
AEPRQRFWRHWLVTDIKGADLKEGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGK
VISLLPKENKTRGSWKMDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKH
KNQAEIAAC"
ORIGIN

Query Match 93.6%; Score 833.2; DB 3; Length 874;
Best Local Similarity 99.0%; Pred. No. 3.5e-235;
Matches 849; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy         24 ACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCTCCCTGTGCTTAACCAGAGG 83
               |||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 ACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCTTCTCCCTGTGCTTAACCAGAGG 60

Qy         84 TGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGG 143
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGG 120

Qy        144 TGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGG 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGG 180

Qy        204 ACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCA 263
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 ACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCA 240

Qy        264 AGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAG 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAG 300

Qy        324 TCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATG 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATG 360

Qy        384 CCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCA 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCA 420

Qy        444 AGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTC 503
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTC 480

Qy        504 CCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAG 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAG 540

Qy        564 GAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACA 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACA 600

Qy        624 GATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGA 683
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGA 660

Qy        684 ACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC- 742
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||| |
Db        661 ACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACA 720

Qy        743 AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCC 802
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCC 780

Qy        803 ACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTT 862
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTT 840

Qy        863 TTCCAAATTAAAAAAAAA 880
              |||||||| |||||||||
Db        841 TTCCAAATAAAAAAAAAA 858


RESULT 2
BU682658/c
LOCUS       BU682658                716 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC1-aci-m-21-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-aci-m-21-0-UI 3', mRNA sequence.
ACCESSION   BU682658
VERSION     BU682658.1  GI:23533769
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 716)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            The following repetitive elements were found in this cDNA
            sequence: 1-42, >POLY_A#Simple_repeat (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .716
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-CF-EC1-aci-m-21-0-UI"
                      /tissue_type="Lung"
                      /dev_stage="Adult and Fetal"
                      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                      /clone_lib="UI-CF-EC1"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      UI-CF-EC1 is a normalized cDNA library containing the
                      following tissue(s): Normal lung from adult and from fetal
                      day 64, day 87, week 19 and week 42. The library was
                      constructed according to Bonaldo, Lennon and Soares,
                      Genome Research, 6:791-806, 1996. First strand cDNA
                      synthesis was primed with an oligo-dT primer containing a
                      Not I site.  Double stranded cDNA was ligated to an EcoR I
                      adaptor, digested with Not I, and cloned directionally
                      into pT7T3-Pac vector. The oligonucleotide used to prime
                      the synthesis of first-strand cDNA contains a library tag
                      sequence that is located between the Not I site and the
                      (dT)18 tail. The sequence tag for this library is
                      AAGTGCTTAC.
                      TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                      and 380-383
                      TAG_LIB=UI-CF-EC1
                      TAG_SEQ=AAGTGCTTAC"
ORIGIN


  Query Match             73.6%;  Score 655;  DB 5;  Length 716;
  Best Local Similarity   98.8%;  Pred. No. 2.2e-182;
  Matches  680;  Conservative    0;  Mismatches    6;  Indels    2;  Gaps    2;

Qy        195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        716 TGGACGAGGACACCCTCTTNTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 657

Qy        255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 597

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 537

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 477

Qy        435 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 417

Qy        495 ACCAGGCTCCC-TCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTAT 553
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ACCAGGCTCCCTTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTAT 357

Qy        554 CTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGG 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 CTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGG 297
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Qy        614 AAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTC 673
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        296 AAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTC 237

Qy        674 ATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAG 733
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        236 ATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAG 177

Qy        734 CCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGG 792
              ||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||
Db        176 CCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGG 117

Qy        793 GCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGA 852
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        116 GCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGA 57

Qy        853 ACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||| |||||||||
Db         56 ACCCCTTCTTTTCCAAATAAAAAAAAA 29


RESULT 3
BG545668
LOCUS       BG545668                749 bp    mRNA    linear   EST 04-APR-2001
DEFINITION  602572933F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4700840 5',
            mRNA sequence.
ACCESSION   BG545668
VERSION     BG545668.1  GI:13544333
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 749)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1535  row: b  column: 09
            High quality sequence stop: 740.
FEATURES             Location/Qualifiers
     source          1. .749
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4700840"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            72.7%;  Score 646.8;  DB 4;  Length 749;
  Best Local Similarity  96.0%;  Pred. No. 5.9e-180;
  Matches  718;  Conservative    0;  Mismatches   22;  Indels    8;  Gaps    5;

Qy          5 ACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCT 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCT 61

Qy         65 CCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG 124
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         62 CCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTTACAGCAGCACTG 121

Qy        125 TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCAT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCAT 181

Qy        185 GAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAG 244
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        182 GAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCA-GGCCTTGAAGTTTTCTACCCAGAG 240

Qy        245 TTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACC 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACC 300

Qy        305 TCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTG 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTG 360

Qy        365 GTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACAT 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACAT 420

Qy        425 TGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAG 484
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        421 TGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAGGAG 480

Qy        485 TTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTC 544
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        481 TTATCAGCCTACCAGGCTCCCTCCCCAACGGCACACAGTGGCTTCCATCGCTACCAGTTC 540

Qy        545 TTTGTCTATCTTCAGGAAGGAA-AAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCG 603
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        541 TTTGTCTATCTTCAGGAAGGAACAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCG 600

Qy        604 AGGCTCTTGGAAAATGGACAGA---TTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC 660
              |||||||||||| |  | || |   ||  ||||||| ||||||||||||||||||||||
Db        601 AGGCTCTTGGAACAATGGCACAGATTTCTTGAACCGGTTCCACCTGGGCGAACCTGAAGC 660

Qy        661 AAGCACCCAGTTCATGA--CCCAGAACTACCAGGACTCA-CCAACCCTCCAGGCTCCCAG 717
              |||||||||||||||||  ||   | |||||||||||| ||||||||||||||||||||
Db        661 AAGCACCCAGTTCATGAACCCAGAACTTACCAGGACTCACCCAACCCTCCAGGCTCCCAG 720

Qy        718 AGGAAGGGCCAGCGAGCCCAAGCACAAA 745
              |||||||||||||||||||     |  |||
Db        721 AGGAAGGGCCAGCGAGCCAGCACCAAAA 748


RESULT 4
BU682973/c
LOCUS       BU682973                685 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC1-acl-g-09-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-acl-g-09-0-UI 3', mRNA sequence.
ACCESSION   BU682973
VERSION     BU682973.1  GI:23534403
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
```

```
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
             The following repetitive elements were found in this cDNA
            sequence: 1-42, >POLY_A#Simple_repeat (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .685
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-acl-g-09-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC1 is a normalized cDNA library containing the
                     following tissue(s): Normal lung from adult and from fetal
                     day 64, day 87, week 19 and week 42. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site.  Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     AAGTGCTTAC.
                     TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                     and 380-383
                     TAG_LIB=UI-CF-EC1
                     TAG_SEQ=AAGTGCTTAC"
ORIGIN

  Query Match             71.6%;  Score 637;  DB 5;  Length 685;
  Best Local Similarity   99.1%;  Pred. No. 4.6e-177;
  Matches  651;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy        225 TTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACA 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACA 626

Qy        285 ACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGG 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 ACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGG 566

Qy        345 ACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCA 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCA 506

Qy        405 GACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAG 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAG 446

Qy        465 GGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTG 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTG 386

Qy        525 GCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTC 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTC 326

Qy        585 CCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACC 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        325 CCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACC 266

Qy        645 TGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCC 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCC 206

Qy        705 TCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTG 763
              ||||||||||||||| |||||||||||||||||||| |||||||||| ||||||||||
Db        205 TCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTG 146

Qy        764 CCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGAT 823
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        145 CCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGAT 86

Qy        824 GTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         85 GTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAAA 29


RESULT 5
BU683324/c
LOCUS       BU683324                681 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC1-ace-m-22-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-ace-m-22-0-UI 3', mRNA sequence.
ACCESSION   BU683324
VERSION     BU683324.1  GI:23535158
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
             The following repetitive elements were found in this cDNA
            sequence: 1-42, >POLY_A#Simple_repeat (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-ace-m-22-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
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UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 70.9%; Score 631.4; DB 5; Length 681;
Best Local Similarity 98.9%; Pred. No. 2.1e-175;
Matches 646; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy      229 AGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTA 288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      681 AGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTA 622

Qy      289 CAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGG 348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      621 CAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGG 562

Qy      349 CGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACA 408
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      561 CGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACA 502

Qy      409 GAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAA 468
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      501 GAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAA 442

Qy      469 GATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTT 528
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      441 GATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTT 382

Qy      529 CCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAA 588
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      381 CCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAA 322

Qy      589 GGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGG 648
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      321 GGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGG 262

Qy      649 CGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCA 708
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      261 CGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCA 202

Qy      709 GGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTG 767
            |||||||||| |||||||||||||||||||||| |||||||||| |||||||||||||||
Db      201 GGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTG 142

Qy      768 CTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGG 827
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      141 CTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGG 82

Qy      828 GTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
            |||||||||||||||||||||||||||||||||||| |||||||||
Db       81 GTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAA 29
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RESULT 6
BU731651/c
LOCUS BU731651 663 bp mRNA linear EST 09-OCT-2002
DEFINITION UI-E-CI1-afr-f-23-0-UI.s1 UI-E-CI1 Homo sapiens cDNA clone UI-E-CI1-afr-f-23-0-UI 3', mRNA sequence.
ACCESSION BU731651
VERSION BU731651.1 GI:23656757
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 663)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-37, >POLY_A#Simple_repeat (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CI1-afr-f-23-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CI1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CI1 is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=RPE and Choroid
TAG_LIB=UI-E-CI1
TAG_SEQ=ACCTA"

ORIGIN

Query Match 69.7%; Score 620; DB 5; Length 663;
Best Local Similarity 99.1%; Pred. No. 5e-172;
Matches 634; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy      242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      663 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 604

Qy      302 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      603 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 544
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Qy        362 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 484

Qy        422 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 424

Qy        482 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 364

Qy        542 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 304

Qy        602 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCA 661
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        303 CGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCA 244

Qy        662 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGA 721
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Db        243 AGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAA 184

Qy        722 AGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC 780
              |||||||||||||||||||| |||||||||| |||||||||||||||||||||||||||
Db        183 AGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGC 124

Qy        781 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC 840
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        123 TTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCC 64

Qy        841 TCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||||||||||||||||| |||||||||
Db         63 TCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAA 24
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RESULT 7
BG203405
LOCUS       BG203405                796 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST22786 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG203405
VERSION     BG203405.1  GI:13725092
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 408.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN
```

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  Query Match             69.2%;  Score 616;  DB 4;  Length 796;
  Best Local Similarity   96.6%;  Pred. No. 8.2e-171;
  Matches  661;  Conservative    0;  Mismatches   20;  Indels    3;  Gaps    3;

Qy         82 GGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGAT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGAT 61

Qy        142 GGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGA 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGA 121

Qy        202 GGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTG 181

Qy        262 CAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGAT 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGAT 241

Qy        322 AGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGA 301

Qy        382 TGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATAT 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATAT 361

Qy        442 CAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGC 421

Qy        502 TCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGA 561
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        422 TCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAAGA 481

Qy        562 AGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGA 621
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        482 AAGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAAATGA 541

Qy        622 CAGATTTCTGAACCGCTTCCACCTGGGCGAA-CCTGAAGCAAGCACCCAGTTCATGACCC 680
              ||||||||| ||||| ||||||||||||||| ||||||| |||||||||||||||||| ||
Db        542 CAGATTTCTTAACCGTTTCCACCTGGGCGAACCCTGAACCAAGCACCCAGTTCATGAACC 601

Qy        681 AGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGC 740
              |||||||||||||||| |||  ||| |||||||||||||| ||||| |  || ||||||||
Db        602 AGAACTACCAGGACTC-CCACACCTTCAGGCTCCCAGAGAAAGGGACCACG-GCCCAAGC 659

Qy        741 ACAAAACCAGGCAGAGATAGCTGC 764
              |||||||||||| ||||    |||
Db        660 ACAAAACCAGGCGGAGAATAGTGC 683
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RESULT 8
CD370545/c
LOCUS       CD370545                729 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT1-bkc-b-15-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bkc-b-15-0-UI 3', mRNA sequence.
ACCESSION   CD370545
VERSION     CD370545.1  GI:31154635
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 729)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bkc-b-15-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                     moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                     vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                     (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                     3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                     3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                     hours; wt adenovirus + LPS 24 hours. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT1
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

  Query Match             69.2%;  Score 615.8;  DB 6;  Length 729;
  Best Local Similarity   96.6%;  Pred. No. 9.1e-171;
  Matches  659;  Conservative    0;  Mismatches   20;  Indels    3;  Gaps    3;

Qy        200 GAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGC 259
              || || || | || ||  |  || | |  | ||||||||||||||||||||||||||||
Db        707 GACGAGACACCCTCTTTGCCAGGGCCTTGAAGTTTCTACCCAGAGTTGGGGAACATTGGC 648

Qy        260 TGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCG 319
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGCAAGG-TGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCG 589

Qy        320 ATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCA 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 ATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCA 529

Qy        380 GATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGAT 439
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 GAT-CCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGAT 470

Qy        440 ATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAG 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 ATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAG 410

Qy        500 GCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 GCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAG 350

Qy        560 GAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATG 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGAAAATG 290

Qy        620 GACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACC 679
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        289 GACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACC 230

Qy        680 CAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAG 739
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        229 CAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAG 170

Qy        740 CAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGT 798
              ||| |||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        169 CACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGT 110

Qy        799 GGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCT 858
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCT 50

Qy        859 TCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||| |||||||||
Db         49 TCTTTTCCAAATAAAAAAAAA 28


RESULT 9
BU678191/c
LOCUS       BU678191                660 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC0-abi-d-12-0-UI.s1 UI-CF-EC0 Homo sapiens cDNA clone
            UI-CF-EC0-abi-d-12-0-UI 3', mRNA sequence.
ACCESSION   BU678191
VERSION     BU678191.1  GI:23524901
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
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          Genetics (www.resgen.com) or from Open Biosystems
          (www.openbiosystems.com).
           The following repetitive elements were found in this cDNA
          sequence: 1-41, >POLY_A#Simple_repeat (matched compliment)
          Seq primer: M13 FORWARD
          POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC0-abi-d-12-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC0"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC0 is a cDNA library containing the following
                     tissue(s): Normal lung from adult and from fetal day 64,
                     day 87, week 19 and week 42. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site.  Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is AAGTGCTTAC.
                     TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                     and 380-383
                     TAG_LIB=UI-CF-EC0
                     TAG_SEQ=AAGTGCTTAC"
ORIGIN

  Query Match             67.6%;  Score 602;  DB 5;  Length 660;
  Best Local Similarity   98.9%;  Pred. No. 1.1e-166;
  Matches  627;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;

Qy        248 GGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCC 307
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        660 GGGAACATTGGCTGCAAGG-TGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCC 602

Qy        308 TGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTG 367
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTG 542

Qy        368 ATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGG 427
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGG 482

Qy        428 CTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTA 487
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTA 422

Qy        488 TCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTT 547
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTT 362

Qy        548 GTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGC 607
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGC 302

Qy        608 TCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACC 667
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        301 TCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACC 242

Qy        668 CAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCC 727
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        241 CAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCC 182

Qy        728 AGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCC 786
              ||||||||||||||| |||||||||| |||||||||||||||||||||||||||||||
Db        181 AGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCC 122

Qy        787 ATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGA 846
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 ATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGA 62

Qy        847 TACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||||||||||| |||||||||
Db         61 TACAGAACCCCTTCTTTTCCAAATAAAAAAAAA 28


RESULT 10
CA440136/c
LOCUS       CA440136                621 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-DT1-awg-l-13-0-UI.s1 NCI_CGAP_DT1 Homo sapiens cDNA clone
            UI-H-DT1-awg-l-13-0-UI 3', mRNA sequence.
ACCESSION   CA440136
VERSION     CA440136.1  GI:24804556
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-35, >POLY_A#Simple_repeat (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-DT1-awg-l-13-0-UI"
                     /tissue_type="Metastatic Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_DT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DT1 is a normalized cDNA library containing the
                     following tissue(s): Metatastic Chondrosarcoma in Lung.
                     The library was constructed according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is AACTGTTCGG.
                     TAG_TISSUE=lung metatastic chondrosarcoma
                     TAG_LIB=UI-H-DT1
                     TAG_SEQ=AACTGTTCGG"
ORIGIN

  Query Match             67.3%;  Score 598.6;  DB 6;  Length 621;
  Best Local Similarity   99.3%;  Pred. No. 1.1e-165;
  Matches  601;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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Qy        286 CTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGA 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGA 562

Qy        346 CGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAG 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 CGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAG 502

Qy        406 ACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGG 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        501 ACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGG 442

Qy        466 GAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGG 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGG 382

Qy        526 CTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCC 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 CTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCC 322

Qy        586 CAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCT 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCT 262

Qy        646 GGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCT 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 GGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCT 202

Qy        706 CCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCC 765
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        201 CCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAAAACCAGGCGGAGATAGCTGCC 142

Qy        766 TGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGT 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGT 82

Qy        826 GGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAAAATCA 22

Qy        886 TCAAA 890
              | ||
Db         21 GCCAA 17
```

RESULT 11
BF852989

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LOCUS       BF852989                603 bp    mRNA    linear   EST 16-JAN-2001
DEFINITION  MR2-EN0093-191200-001-a12 EN0093 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF852989
VERSION     BF852989.1  GI:12240837
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-EN0093-
            191200-001-a12&t3=2000-12-19&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1. .603
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="EN0093"
                     /note="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN
```

Query Match 65.6%; Score 584; DB 2; Length 603;
Best Local Similarity 98.3%; Pred. No. 2.3e-161;
Matches 590; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy          2 AGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCT 61
              | |||||||||||||||||||||||||||||||| ||||||||||||||||||||| ||||
Db          4 AATACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCT 63

Qy         62 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 TCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCA 123

Qy        122 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 CTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCC 183

Qy        182 CATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 241
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        184 CATGAGGCCCTCTTGAACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCA 243

Qy        242 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GAGTTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATC 303

Qy        302 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATC 363

Qy        362 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGA 423

Qy        422 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAG 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        424 CATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGGCAG 483

Qy        482 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAG 541
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        484 GAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTAACAG 543

Qy        542 TTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACT 601
              |||||||||||||||||||| ||| |||||||||||||||| |||||| ||||||||||
Db        544 TTCTTTGTCTATCTTCAGGGAGGGAAAGTCATCTCTCTCCTTTCCAAGGGAAACAAAACT 603
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RESULT 12
BU680465/c

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LOCUS       BU680465                620 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC1-abl-d-09-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-abl-d-09-0-UI 3', mRNA sequence.
ACCESSION   BU680465
VERSION     BU680465.1  GI:23529424
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
             The following repetitive elements were found in this cDNA
            sequence: 1-38, >POLY_A#Simple_repeat (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-abl-d-09-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC1 is a normalized cDNA library containing the
                     following tissue(s): Normal lung from adult and from fetal
                     day 64, day 87, week 19 and week 42. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site.  Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     AAGTGCTTAC.
                     TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                     and 380-383
                     TAG_LIB=UI-CF-EC1
                     TAG_SEQ=AAGTGCTTAC"
ORIGIN

  Query Match             64.7%;  Score 576;  DB 5;  Length 620;
  Best Local Similarity   99.0%;  Pred. No. 5.4e-159;
  Matches  590;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy        286 CTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGA 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGA 561

Qy        346 CGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAG 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 CGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAG 501

Qy        406 ACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGG 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 ACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGG 441

Qy        466 GAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGG 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 GAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGG 381

Qy        526 CTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCC 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCC 321

Qy        586 CAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCT 645
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        320 CAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGTTTCCACCT 261

Qy        646 GGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCT 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCT 201

Qy        706 CCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGC 764
              |||||||||||||| |||||||||||||||||||||| |||||||||| ||||||||||
Db        200 CCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGC 141

Qy        765 CTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATG 824
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        140 CTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATG 81

Qy        825 TGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         80 TGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAAA 25


RESULT 13
BP216854
LOCUS       BP216854                581 bp    mRNA    linear   EST 15-SEP-2004
DEFINITION  BP216854 Sugano cDNA library, corpus callosum Homo sapiens cDNA
            clone CCR08207, mRNA sequence.
ACCESSION   BP216854
VERSION     BP216854.1  GI:52089755
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CCR08207"
                     /tissue_type="corpus callosum"
                     /clone_lib="Sugano cDNA library, corpus callosum"
ORIGIN

  Query Match             64.4%;  Score 573;  DB 5;  Length 581;
  Best Local Similarity   99.1%;  Pred. No. 4.1e-158;
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  Matches  576;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 ACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCT 64
              ||||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Db          1 ACTTGTGTCCGGGTGGTGGACTGGATTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCTTCT 60

Qy         65 CCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG 120

Qy        125 TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCAT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCAT 180

Qy        185 GAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAG 240

Qy        245 TTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACC 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGGGGAACATTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACC 300

Qy        305 TCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTG 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTG 360

Qy        365 GTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACAT 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACAT 420

Qy        425 TGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAG 484
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        421 TGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGATTCAGGGCCAGGAG 480

Qy        485 TTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTC 540

Qy        545 TTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCC 585
              |||||||||||||||| ||| ||||||||||||||||||||
Db        541 TTTGTCTATCTTCAGGGAGGGAAAGTCATCTCTCTCCTTCC 581
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```
RESULT 14
BM984582/c
LOCUS       BM984582                624 bp    mRNA    linear   EST 20-FEB-2003
DEFINITION  UI-CF-EC1-abj-k-03-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-abj-k-03-0-UI 3', mRNA sequence.
ACCESSION   BM984582
VERSION     BM984582.1  GI:19610241
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
             The following repetitive elements were found in this cDNA
            sequence: 1-42, >POLY_A#Simple_repeat (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-abj-k-03-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC1 is a normalized cDNA library containing the
                     following tissue(s): Normal lung from adult and from fetal
                     day 64, day 87, week 19 and week 42. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site.  Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     AAGTGCTTAC.
                     TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                     and 380-383
                     TAG_LIB=UI-CF-EC1
                     TAG_SEQ=AAGTGCTTAC"
ORIGIN
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  Query Match             64.4%;  Score 572.8;  DB 5;  Length 624;
  Best Local Similarity   98.7%;  Pred. No. 4.8e-158;
  Matches  588;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy        286 CTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGA 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGA 565

Qy        346 CGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAG 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAG 505

Qy        406 ACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGG 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        504 ACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGG 445

Qy        466 GAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGG 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGG 385

Qy        526 CTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCC 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCC 325

Qy        586 CAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCT 645
              |||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||
Db        324 CAAGGAAAACAAAACTCGAGGCTCTTGGAAAATGGACAGATTTTTGAACCGTTTCCACCT 265

Qy        646 GGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCT 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCT 205

Qy        706 CCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCAC-AAAACCAGGCAGAGATAGCTGC 764
              |||||||||||||| |||||||||||||||||||||| |||||||||| ||||||||||
Db        204 CCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCACAAAAACCAGGCGGAGATAGCTGC 145
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Qy        765 CTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATG 824
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        144 CTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACACTGCCCACCACCGACGATG 85

Qy        825 TGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         84 TGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAAAAA 29


RESULT 15
BP316275
LOCUS       BP316275                582 bp    mRNA    linear   EST 17-SEP-2004
DEFINITION  BP316275 Sugano cDNA library, pericardium Homo sapiens cDNA clone
            PCD00918, mRNA sequence.
ACCESSION   BP316275
VERSION     BP316275.1  GI:52245250
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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ORIGIN

  Query Match             62.5%;  Score 556.6;  DB 5;  Length 582;
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  Matches  573;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy         27 GGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCTCCCTGTGCTTAACCAGAGGTGC 86
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Db          1 GGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTTCTCCCTGTGCTTAACCAGAGGTGC 60

Qy         87 CCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGGTGG 146
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 CCATGGGTTGGACAATGAGGCTGGTCACAGCATCACTGTTACTGGGTCTCATGATGGTGG 120

Qy        147 TCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGGACA 206
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 GCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGTACGAGGACA 180

Qy        207 CCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGG 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGCTGCAAGG 240

Qy        267 TTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCA 326
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        241 TTGTTCCTGATTGTAACAACTACAGACAGATGATCACCTCCTGGATGGAGCCGATAGTCA 300

Qy        327 AGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCC 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCC 360

Qy        387 CTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGG 446
              |||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||

Db        361 CTAGCAGAGCATAACCCAGACAGAGATTCTGGAGACATTGGCTGCTAACAGATATCAAGG 420

Qy        447 GCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCT 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCT 480

Qy        507 CCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGAAGGAA 566
              || |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        481 CCTCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCATGAAGGAA 540

Qy        567 AAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTC 609
              |||||||||||||||||||| ||| ||||||||||||||||
Db        541 AAGTCATCTCTCTCCTTCCCAA-GAATACAAAACTCGAGGCTC 582


Search completed: July 24, 2005, 01:17:49
Job time : 5019 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 23:03:18 ; Search time 260 Seconds
(without alignments)
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Title: US-10-036-214-60
Perfect score: 890
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	858.4	96.4	903	3	US-09-208-718-4	Sequence 4, Appli
	2	783.8	88.1	826	4	US-09-621-976-7	Sequence 7, Appli
	3	783.8	88.1	826	4	US-09-513-999C-7	Sequence 7, Appli
	4	783.8	88.1	826	4	US-09-471-276-7	Sequence 7, Appli
	5	45.4	5.1	1047	1	US-08-403-378B-3	Sequence 3, Appli
	6	41	4.6	916	4	US-09-799-451-460	Sequence 460, App
	7	41	4.6	1447	1	US-08-403-378B-14	Sequence 14, Appl
	8	39	4.4	660	4	US-09-252-991A-2742	Sequence 2742, Ap
c	9	39	4.4	768	4	US-09-252-991A-3027	Sequence 3027, Ap
	10	39	4.4	1671	4	US-09-252-991A-2839	Sequence 2839, Ap
c	11	39	4.4	2352	4	US-09-252-991A-3127	Sequence 3127, Ap
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	13	37.6	4.2	2441	4	US-09-949-016-29	Sequence 29, Appl
	14	36.8	4.1	855	3	US-09-060-726A-1	Sequence 1, Appli
c	15	36.8	4.1	856	3	US-09-060-726A-3	Sequence 3, Appli
	16	36.8	4.1	856	4	US-09-845-849A-1	Sequence 1, Appli
c	17	36.8	4.1	856	4	US-09-845-849A-3	Sequence 3, Appli
	18	35	3.9	1635	4	US-09-902-540-8993	Sequence 8993, Ap
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	20	35	3.9	10692	4	US-09-902-540-960	Sequence 960, App
c	21	34.6	3.9	7661	4	US-09-949-016-14822	Sequence 14822, A
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	32	33.4	3.8	601	4	US-09-949-016-58357	Sequence 58357, A
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	35	33.4	3.8	36542	4	US-09-949-016-12149	Sequence 12149, A
	36	33.4	3.8	36544	4	US-09-949-016-13434	Sequence 13434, A
	37	33.2	3.7	897	4	US-09-949-016-2018	Sequence 2018, Ap
c	38	33.2	3.7	219964	4	US-09-949-016-15086	Sequence 15086, A
	39	32.8	3.7	282	4	US-09-313-294A-6772	Sequence 6772, Ap
	40	32.8	3.7	601	4	US-09-949-016-120352	Sequence 120352,
	41	32.8	3.7	601	4	US-09-949-016-120353	Sequence 120353,
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	44	32.6	3.7	601	4	US-09-949-016-174609	Sequence 174609,
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	63	31.8	3.6	601	4	US-09-949-016-180162	Sequence 180162,
	64	31.8	3.6	780	4	US-09-252-991A-12515	Sequence 12515, A
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	67	31.8	3.6	11301	4	US-09-902-540-1046	Sequence 1046, Ap
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	76	31.6	3.6	4533	3	US-08-726-214-5	Sequence 5, Appli
	77	31.6	3.6	11963	4	US-09-902-540-1072	Sequence 1072, Ap
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	86	31.4	3.5	750	4	US-09-389-681-58	Sequence 58, Appl
	87	31.4	3.5	750	4	US-09-620-405B-58	Sequence 58, Appl
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	89	31.4	3.5	750	4	US-09-433-826B-58	Sequence 58, Appl
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	92	31.4	3.5	750	4	US-09-834-759-58	Sequence 58, Appl
	93	31.4	3.5	750	4	US-09-590-751A-58	Sequence 58, Appl
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	109	31.2	3.5	112508	4	US-09-949-016-16589	Sequence 16589, A
	110	31.2	3.5	112508	4	US-09-949-016-16590	Sequence 16590, A
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	142	30.8	3.5	18331	4	US-09-266-965-96	Sequence 96, Appl
	143	30.8	3.5	70828	4	US-09-949-016-12122	Sequence 12122, A
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c	155	30.4	3.4	601	4	US-09-949-016-160527	Sequence 160527,
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	159	30.4	3.4	30782	4	US-09-949-016-13724	Sequence 13724, A
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	172	30.2	3.4	1155	4	US-09-949-016-2638	Sequence 2638, Ap
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	232	29.8	3.3	4080	4	US-09-016-434-1326	Sequence 1326, Ap
	233	29.8	3.3	5645	4	US-09-023-655-1319	Sequence 1319, Ap
	234	29.8	3.3	5681	4	US-09-919-172-58	Sequence 58, Appl
	235	29.8	3.3	5933	4	US-09-919-172-23	Sequence 23, Appl
	236	29.8	3.3	16782	4	US-09-902-540-1105	Sequence 1105, Ap
	237	29.8	3.3	23901	4	US-09-949-016-16773	Sequence 16773, A
c	238	29.8	3.3	39920	4	US-09-949-016-16316	Sequence 16316, A
c	239	29.8	3.3	51927	4	US-09-949-016-17347	Sequence 17347, A
c	240	29.8	3.3	51927	4	US-09-949-016-17348	Sequence 17348, A
c	241	29.8	3.3	73853	4	US-09-949-016-12029	Sequence 12029, A
	242	29.8	3.3	96690	4	US-09-949-016-17103	Sequence 17103, A
	243	29.8	3.3	116592	4	US-09-818-512-3	Sequence 3, Appli
	244	29.8	3.3	124264	4	US-09-949-016-16396	Sequence 16396, A
c	245	29.6	3.3	297	3	US-09-493-565-3	Sequence 3, Appli
c	246	29.6	3.3	478	4	US-09-585-173B-5	Sequence 5, Appli

c 247	29.6	3.3	532	4	US-09-621-976-2170	Sequence 2170, Ap
c 248	29.6	3.3	601	4	US-09-949-016-77374	Sequence 77374, A
c 249	29.6	3.3	601	4	US-09-949-016-77375	Sequence 77375, A
c 250	29.6	3.3	601	4	US-09-949-016-105241	Sequence 105241,
251	29.6	3.3	601	4	US-09-949-016-117409	Sequence 117409,
c 252	29.6	3.3	601	4	US-09-949-016-138299	Sequence 138299,
253	29.6	3.3	1155	4	US-09-252-991A-5158	Sequence 5158, Ap
c 254	29.6	3.3	1233	4	US-09-252-991A-5057	Sequence 5057, Ap
255	29.6	3.3	2016	3	US-09-132-118-1	Sequence 1, Appli
c 256	29.6	3.3	2130	4	US-09-949-016-1037	Sequence 1037, Ap
257	29.6	3.3	2137	1	US-08-444-005-16	Sequence 16, Appl
c 258	29.6	3.3	2156	4	US-09-949-016-3769	Sequence 3769, Ap
259	29.6	3.3	2550	4	US-09-949-016-4927	Sequence 4927, Ap
260	29.6	3.3	2617	3	US-09-161-443-1	Sequence 1, Appli
261	29.6	3.3	2617	4	US-09-023-655-914	Sequence 914, App
262	29.6	3.3	9687	3	US-09-133-944-2	Sequence 2, Appli
263	29.6	3.3	9687	3	US-09-208-827-2	Sequence 2, Appli
264	29.6	3.3	9687	4	US-10-043-074-2	Sequence 2, Appli
265	29.6	3.3	11874	4	US-09-949-016-17115	Sequence 17115, A
c 266	29.6	3.3	19700	4	US-09-949-016-12618	Sequence 12618, A
267	29.6	3.3	63183	4	US-09-949-016-13047	Sequence 13047, A
268	29.6	3.3	63183	4	US-09-949-016-13048	Sequence 13048, A
c 269	29.6	3.3	72128	4	US-09-949-016-16018	Sequence 16018, A
270	29.6	3.3	114842	4	US-09-949-016-14993	Sequence 14993, A
271	29.6	3.3	153642	4	US-09-949-016-12174	Sequence 12174, A
272	29.6	3.3	153643	4	US-09-949-016-15635	Sequence 15635, A
c 273	29.6	3.3	154626	4	US-09-949-016-14000	Sequence 14000, A
c 274	29.6	3.3	346112	4	US-09-949-016-13165	Sequence 13165, A
275	29.4	3.3	349	4	US-09-513-999C-1236	Sequence 1236, Ap
276	29.4	3.3	601	4	US-09-949-016-24335	Sequence 24335, A
277	29.4	3.3	601	4	US-09-949-016-24336	Sequence 24336, A
278	29.4	3.3	601	4	US-09-949-016-32352	Sequence 32352, A
279	29.4	3.3	601	4	US-09-949-016-32353	Sequence 32353, A
c 280	29.4	3.3	601	4	US-09-949-016-104812	Sequence 104812,
c 281	29.4	3.3	601	4	US-09-949-016-104859	Sequence 104859,
282	29.4	3.3	601	4	US-09-949-016-137160	Sequence 137160,
283	29.4	3.3	601	4	US-09-949-016-137161	Sequence 137161,
284	29.4	3.3	601	4	US-09-949-016-137186	Sequence 137186,
285	29.4	3.3	601	4	US-09-949-016-137187	Sequence 137187,
c 286	29.4	3.3	601	4	US-09-949-016-166950	Sequence 166950,
c 287	29.4	3.3	601	4	US-09-949-016-166970	Sequence 166970,
288	29.4	3.3	1104	4	US-09-464-035A-10	Sequence 10, Appl
c 289	29.4	3.3	1140	4	US-09-540-236-1296	Sequence 1296, Ap
290	29.4	3.3	1194	4	US-09-902-540-3833	Sequence 3833, Ap
c 291	29.4	3.3	1659	4	US-09-248-796A-1820	Sequence 1820, Ap
c 292	29.4	3.3	1946	3	US-09-042-225-5	Sequence 5, Appli
293	29.4	3.3	2034	4	US-09-963-137-152	Sequence 152, App
c 294	29.4	3.3	3891	2	US-08-969-630-3	Sequence 3, Appli
c 295	29.4	3.3	19091	4	US-09-949-016-15805	Sequence 15805, A
296	29.4	3.3	20757	4	US-09-902-540-1189	Sequence 1189, Ap
c 297	29.4	3.3	21978	4	US-09-949-016-16646	Sequence 16646, A
298	29.4	3.3	23292	4	US-09-949-016-12100	Sequence 12100, A
299	29.4	3.3	23292	4	US-09-949-016-13205	Sequence 13205, A
300	29.4	3.3	38371	4	US-09-949-016-12061	Sequence 12061, A
301	29.4	3.3	38371	4	US-09-949-016-12488	Sequence 12488, A
302	29.4	3.3	38371	4	US-09-949-016-15596	Sequence 15596, A
303	29.4	3.3	38371	4	US-09-949-016-15597	Sequence 15597, A
c 304	29.4	3.3	43117	4	US-09-949-016-17589	Sequence 17589, A
c 305	29.4	3.3	57859	4	US-09-949-016-12334	Sequence 12334, A
c 306	29.4	3.3	57859	4	US-09-949-016-14657	Sequence 14657, A
c 307	29.4	3.3	57859	4	US-09-949-016-14658	Sequence 14658, A
c 308	29.4	3.3	75674	4	US-09-949-016-17597	Sequence 17597, A
c 309	29.4	3.3	83178	4	US-09-949-016-14606	Sequence 14606, A
310	29.4	3.3	87648	4	US-09-949-016-13655	Sequence 13655, A
311	29.4	3.3	92407	4	US-09-596-002-36	Sequence 36, Appl
312	29.2	3.3	437	3	US-09-091-725-46	Sequence 46, Appl
c 313	29.2	3.3	522	1	US-08-672-569-3	Sequence 3, Appli
c 314	29.2	3.3	552	4	US-09-489-039A-5671	Sequence 5671, Ap
315	29.2	3.3	601	4	US-09-949-016-147778	Sequence 147778,
316	29.2	3.3	609	4	US-09-621-976-3500	Sequence 3500, Ap
317	29.2	3.3	639	4	US-09-489-039A-5903	Sequence 5903, Ap
c 318	29.2	3.3	817	1	US-08-672-569-2	Sequence 2, Appli
c 319	29.2	3.3	861	4	US-09-489-039A-5536	Sequence 5536, Ap
c 320	29.2	3.3	1116	1	US-08-672-569-1	Sequence 1, Appli
321	29.2	3.3	1194	4	US-09-489-039A-3387	Sequence 3387, Ap
322	29.2	3.3	1410	4	US-09-489-039A-6394	Sequence 6394, Ap
323	29.2	3.3	1482	4	US-09-977-897-1	Sequence 1, Appli
324	29.2	3.3	1686	4	US-09-724-797-9	Sequence 9, Appli
c 325	29.2	3.3	2582	2	US-08-816-105A-2	Sequence 2, Appli
c 326	29.2	3.3	3666	4	US-09-976-594-303	Sequence 303, App
327	29.2	3.3	3761	4	US-09-902-540-556	Sequence 556, App
328	29.2	3.3	4631	4	US-09-620-312D-164	Sequence 164, App
329	29.2	3.3	12425	4	US-09-616-289-50	Sequence 50, Appl
330	29.2	3.3	16154	4	US-09-949-016-16669	Sequence 16669, A
c 331	29.2	3.3	16782	4	US-09-902-540-1105	Sequence 1105, Ap
c 332	29.2	3.3	23501	4	US-09-949-016-17517	Sequence 17517, A
c 333	29.2	3.3	61158	4	US-09-949-016-15041	Sequence 15041, A
c 334	29.2	3.3	74644	4	US-09-949-016-17556	Sequence 17556, A
c 335	29.2	3.3	75431	4	US-09-949-016-15122	Sequence 15122, A
336	29.2	3.3	86414	4	US-09-949-016-12345	Sequence 12345, A
337	29.2	3.3	86414	4	US-09-949-016-15758	Sequence 15758, A
338	29.2	3.3	87216	4	US-09-949-016-15891	Sequence 15891, A
c 339	29.2	3.3	137226	4	US-09-949-016-13763	Sequence 13763, A
340	29.2	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 341	29.2	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
342	29.2	3.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 343	29.2	3.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 344	29	3.3	601	4	US-09-949-016-65454	Sequence 65454, A
c 345	29	3.3	601	4	US-09-949-016-69363	Sequence 69363, A
c 346	29	3.3	601	4	US-09-949-016-79430	Sequence 79430, A
c 347	29	3.3	601	4	US-09-949-016-79431	Sequence 79431, A
348	29	3.3	601	4	US-09-949-016-174562	Sequence 174562,
349	29	3.3	601	4	US-09-949-016-182921	Sequence 182921,
c 350	29	3.3	738	4	US-09-252-991A-14821	Sequence 14821, A
c 351	29	3.3	1164	4	US-09-252-991A-1799	Sequence 1799, Ap
c 352	29	3.3	1299	4	US-09-799-451-944	Sequence 944, App
353	29	3.3	1302	4	US-09-252-991A-2166	Sequence 2166, Ap
354	29	3.3	1341	4	US-09-252-991A-14543	Sequence 14543, A
c 355	29	3.3	1531	3	US-08-630-915A-21	Sequence 21, Appl
c 356	29	3.3	1531	4	US-09-879-957-21	Sequence 21, Appl
357	29	3.3	1746	4	US-09-252-991A-15790	Sequence 15790, A
c 358	29	3.3	2064	4	US-09-252-991A-15079	Sequence 15079, A
359	29	3.3	2370	4	US-09-252-991A-12196	Sequence 12196, A
c 360	29	3.3	3036	4	US-09-252-991A-15848	Sequence 15848, A
c 361	29	3.3	3120	4	US-09-252-991A-12395	Sequence 12395, A
c 362	29	3.3	4078	4	US-09-016-434-1154	Sequence 1154, Ap
c 363	29	3.3	5430	4	US-09-949-016-12493	Sequence 12493, A
c 364	29	3.3	5435	4	US-09-949-016-13286	Sequence 13286, A
365	29	3.3	34030	4	US-09-949-016-12248	Sequence 12248, A
366	29	3.3	34031	4	US-09-949-016-13540	Sequence 13540, A
c 367	29	3.3	49399	4	US-09-949-016-13780	Sequence 13780, A
368	29	3.3	51967	4	US-09-949-016-16982	Sequence 16982, A
369	29	3.3	61847	4	US-09-949-016-16677	Sequence 16677, A
370	29	3.3	109159	4	US-09-949-016-14169	Sequence 14169, A
371	29	3.3	109159	4	US-09-949-016-14170	Sequence 14170, A
c 372	29	3.3	784019	4	US-09-949-016-14033	Sequence 14033, A
c 373	29	3.3	828152	4	US-09-949-016-12777	Sequence 12777, A
c 374	28.8	3.2	293	4	US-09-902-540-7264	Sequence 7264, Ap
c 375	28.8	3.2	417	4	US-09-252-991A-4583	Sequence 4583, Ap
c 376	28.8	3.2	533	4	US-09-389-681-271	Sequence 271, App
c 377	28.8	3.2	533	4	US-09-620-405B-271	Sequence 271, App
c 378	28.8	3.2	533	4	US-09-339-338-271	Sequence 271, App
c 379	28.8	3.2	533	4	US-09-433-826B-271	Sequence 271, App
c 380	28.8	3.2	533	4	US-09-604-287A-271	Sequence 271, App
c 381	28.8	3.2	533	4	US-09-834-759-271	Sequence 271, App
c 382	28.8	3.2	533	4	US-09-590-751A-271	Sequence 271, App
c 383	28.8	3.2	533	4	US-09-551-621-271	Sequence 271, App
c 384	28.8	3.2	601	4	US-09-949-016-53631	Sequence 53631, A
385	28.8	3.2	601	4	US-09-949-016-138711	Sequence 138711,
c 386	28.8	3.2	601	4	US-09-949-016-206227	Sequence 206227,
387	28.8	3.2	606	4	US-09-252-991A-4784	Sequence 4784, Ap
388	28.8	3.2	636	4	US-09-489-039A-5274	Sequence 5274, Ap
389	28.8	3.2	647	2	US-08-997-080-115	Sequence 115, App
390	28.8	3.2	647	2	US-08-997-362-115	Sequence 115, App
391	28.8	3.2	647	3	US-09-095-855-115	Sequence 115, App
392	28.8	3.2	647	3	US-09-324-542-115	Sequence 115, App

393	28.8	3.2	647	3	US-09-205-426-115	Sequence 115, App
394	28.8	3.2	668	4	US-09-492-308A-4	Sequence 4, Appli
395	28.8	3.2	668	4	US-09-492-308A-16	Sequence 16, Appl
396	28.8	3.2	668	4	US-09-492-308A-18	Sequence 18, Appl
397	28.8	3.2	675	4	US-09-902-540-3775	Sequence 3775, Ap
398	28.8	3.2	680	4	US-09-492-308A-9	Sequence 9, Appli
c 399	28.8	3.2	1355	4	US-09-870-472A-10	Sequence 10, Appl
400	28.8	3.2	1419	4	US-09-252-991A-10421	Sequence 10421, A
401	28.8	3.2	1569	2	US-08-997-080-113	Sequence 113, App
402	28.8	3.2	1569	2	US-08-997-362-113	Sequence 113, App
403	28.8	3.2	1569	3	US-09-095-855-113	Sequence 113, App
404	28.8	3.2	1569	3	US-09-324-542-113	Sequence 113, App
405	28.8	3.2	1569	3	US-09-205-426-113	Sequence 113, App
406	28.8	3.2	1626	2	US-08-997-080-159	Sequence 159, App
407	28.8	3.2	1626	2	US-08-997-362-159	Sequence 159, App
408	28.8	3.2	1626	3	US-09-095-855-159	Sequence 159, App
409	28.8	3.2	1626	3	US-09-324-542-159	Sequence 159, App
410	28.8	3.2	1626	3	US-09-205-426-159	Sequence 159, App
411	28.8	3.2	1695	4	US-09-252-991A-10319	Sequence 10319, A
c 412	28.8	3.2	1995	3	US-08-904-452-1	Sequence 1, Appli
c 413	28.8	3.2	1995	3	US-09-517-639-1	Sequence 1, Appli
414	28.8	3.2	2130	4	US-09-425-335-1	Sequence 1, Appli
c 415	28.8	3.2	2376	4	US-09-252-991A-10741	Sequence 10741, A
416	28.8	3.2	2878	4	US-09-917-963-10	Sequence 10, Appl
c 417	28.8	3.2	3069	4	US-09-514-907A-5	Sequence 5, Appli
c 418	28.8	3.2	3069	4	US-09-896-994-5	Sequence 5, Appli
c 419	28.8	3.2	3135	4	US-09-902-540-5547	Sequence 5547, Ap
420	28.8	3.2	3456	4	US-09-252-991A-4757	Sequence 4757, Ap
c 421	28.8	3.2	3684	4	US-09-902-540-683	Sequence 683, App
c 422	28.8	3.2	23233	4	US-09-902-540-1184	Sequence 1184, Ap
423	28.8	3.2	23569	4	US-09-949-016-12153	Sequence 12153, A
424	28.8	3.2	23574	4	US-09-949-016-15351	Sequence 15351, A
c 425	28.8	3.2	25254	4	US-09-902-540-1233	Sequence 1233, Ap
c 426	28.8	3.2	29965	4	US-09-949-016-11953	Sequence 11953, A
c 427	28.8	3.2	29966	4	US-09-949-016-16728	Sequence 16728, A
c 428	28.8	3.2	41170	4	US-09-902-540-1267	Sequence 1267, Ap
c 429	28.8	3.2	105210	4	US-09-949-016-14158	Sequence 14158, A
430	28.8	3.2	116955	4	US-09-949-016-17565	Sequence 17565, A
c 431	28.8	3.2	120609	4	US-09-949-016-13915	Sequence 13915, A
432	28.8	3.2	194889	4	US-09-949-016-15654	Sequence 15654, A
c 433	28.6	3.2	274	4	US-09-313-294A-2249	Sequence 2249, Ap
434	28.6	3.2	601	4	US-09-949-016-46848	Sequence 46848, A
435	28.6	3.2	601	4	US-09-949-016-46850	Sequence 46850, A
436	28.6	3.2	601	4	US-09-949-016-46851	Sequence 46851, A
c 437	28.6	3.2	601	4	US-09-949-016-49734	Sequence 49734, A
c 438	28.6	3.2	843	4	US-09-902-540-9093	Sequence 9093, Ap
c 439	28.6	3.2	1002	4	US-09-902-540-3214	Sequence 3214, Ap
c 440	28.6	3.2	3577	4	US-09-620-312D-457	Sequence 457, App
c 441	28.6	3.2	4196	4	US-09-774-528-236	Sequence 236, App
442	28.6	3.2	7188	4	US-10-101-957B-1	Sequence 1, Appli
443	28.6	3.2	10915	4	US-09-902-540-972	Sequence 972, App
444	28.6	3.2	16738	4	US-09-949-016-12168	Sequence 12168, A
c 445	28.6	3.2	16738	4	US-09-949-016-12168	Sequence 12168, A
446	28.6	3.2	16738	4	US-09-949-016-14678	Sequence 14678, A
c 447	28.6	3.2	16738	4	US-09-949-016-14678	Sequence 14678, A
448	28.6	3.2	19455	4	US-09-902-540-1147	Sequence 1147, Ap
c 449	28.6	3.2	28438	4	US-09-820-790B-3	Sequence 3, Appli
c 450	28.6	3.2	28555	4	US-09-949-016-13106	Sequence 13106, A
c 451	28.6	3.2	57280	4	US-09-949-016-11796	Sequence 11796, A
c 452	28.6	3.2	57280	4	US-09-949-016-12843	Sequence 12843, A
c 453	28.6	3.2	57280	4	US-09-949-016-12844	Sequence 12844, A
c 454	28.6	3.2	57280	4	US-09-949-016-12846	Sequence 12846, A
c 455	28.6	3.2	57280	4	US-09-949-016-13542	Sequence 13542, A
c 456	28.6	3.2	57280	4	US-09-949-016-13543	Sequence 13543, A
c 457	28.6	3.2	57280	4	US-09-949-016-13544	Sequence 13544, A
c 458	28.6	3.2	57280	4	US-09-949-016-13545	Sequence 13545, A
c 459	28.6	3.2	57280	4	US-09-949-016-14633	Sequence 14633, A
c 460	28.6	3.2	57280	4	US-09-949-016-14634	Sequence 14634, A
c 461	28.6	3.2	57280	4	US-09-949-016-14635	Sequence 14635, A
c 462	28.6	3.2	57280	4	US-09-949-016-14636	Sequence 14636, A
c 463	28.6	3.2	57280	4	US-09-949-016-14637	Sequence 14637, A
c 464	28.6	3.2	57280	4	US-09-949-016-14638	Sequence 14638, A
c 465	28.6	3.2	57280	4	US-09-949-016-14639	Sequence 14639, A
c 466	28.6	3.2	57280	4	US-09-949-016-14640	Sequence 14640, A
467	28.6	3.2	57392	4	US-09-949-016-12070	Sequence 12070, A
468	28.6	3.2	57402	4	US-09-949-016-13293	Sequence 13293, A
c 469	28.6	3.2	71879	4	US-09-949-016-17465	Sequence 17465, A
c 470	28.6	3.2	126200	4	US-09-949-016-11824	Sequence 11824, A
c 471	28.6	3.2	126200	4	US-09-949-016-13193	Sequence 13193, A
c 472	28.6	3.2	128516	4	US-09-949-016-13501	Sequence 13501, A
c 473	28.6	3.2	133157	4	US-09-949-016-12541	Sequence 12541, A
c 474	28.6	3.2	141560	4	US-09-949-016-16476	Sequence 16476, A
c 475	28.4	3.2	601	4	US-09-949-016-55191	Sequence 55191, A
c 476	28.4	3.2	601	4	US-09-949-016-55192	Sequence 55192, A
c 477	28.4	3.2	601	4	US-09-949-016-84380	Sequence 84380, A
c 478	28.4	3.2	601	4	US-09-949-016-105242	Sequence 105242,
479	28.4	3.2	601	4	US-09-949-016-120630	Sequence 120630,
c 480	28.4	3.2	601	4	US-09-949-016-152356	Sequence 152356,
481	28.4	3.2	846	3	US-08-748-547-3	Sequence 3, Appli
c 482	28.4	3.2	937	4	US-09-270-767-26154	Sequence 26154, A
c 483	28.4	3.2	1026	4	US-09-270-767-10701	Sequence 10701, A
c 484	28.4	3.2	1134	4	US-09-252-991A-16395	Sequence 16395, A
485	28.4	3.2	1218	4	US-09-252-991A-3419	Sequence 3419, Ap
c 486	28.4	3.2	1404	4	US-09-252-991A-8470	Sequence 8470, Ap
487	28.4	3.2	1497	2	US-08-432-693-10	Sequence 10, Appl
488	28.4	3.2	1497	4	US-09-949-016-89	Sequence 89, Appl
489	28.4	3.2	1498	4	US-09-949-016-5491	Sequence 5491, Ap
490	28.4	3.2	1514	2	US-08-483-806-1	Sequence 1, Appli
c 491	28.4	3.2	1545	4	US-09-902-540-9680	Sequence 9680, Ap
c 492	28.4	3.2	1587	4	US-09-252-991A-16504	Sequence 16504, A
493	28.4	3.2	1647	4	US-09-252-991A-3344	Sequence 3344, Ap
494	28.4	3.2	1743	4	US-09-919-172-26	Sequence 26, Appl
495	28.4	3.2	1842	4	US-09-252-991A-8411	Sequence 8411, Ap
c 496	28.4	3.2	2040	2	US-08-533-669A-5	Sequence 5, Appli
c 497	28.4	3.2	2040	3	US-09-183-861-5	Sequence 5, Appli
c 498	28.4	3.2	2040	3	US-09-022-765-5	Sequence 5, Appli
c 499	28.4	3.2	2040	4	US-09-551-974A-5	Sequence 5, Appli
c 500	28.4	3.2	2040	4	US-09-565-501A-5	Sequence 5, Appli
c 501	28.4	3.2	2040	4	US-09-639-206A-5	Sequence 5, Appli
c 502	28.4	3.2	2040	4	US-09-874-923-5	Sequence 5, Appli
c 503	28.4	3.2	2040	4	US-08-798-841-5	Sequence 5, Appli
c 504	28.4	3.2	4233	4	US-09-551-974A-99	Sequence 99, Appl
c 505	28.4	3.2	4233	4	US-09-565-501A-99	Sequence 99, Appl
c 506	28.4	3.2	4233	4	US-09-639-206A-99	Sequence 99, Appl
c 507	28.4	3.2	4233	4	US-09-874-923-99	Sequence 99, Appl
c 508	28.4	3.2	4917	4	US-09-551-974A-100	Sequence 100, App
c 509	28.4	3.2	4917	4	US-09-565-501A-100	Sequence 100, App
c 510	28.4	3.2	4917	4	US-09-639-206A-100	Sequence 100, App
c 511	28.4	3.2	4917	4	US-09-874-923-100	Sequence 100, App
c 512	28.4	3.2	4929	4	US-09-551-974A-98	Sequence 98, Appl
c 513	28.4	3.2	4929	4	US-09-565-501A-98	Sequence 98, Appl
c 514	28.4	3.2	4929	4	US-09-639-206A-98	Sequence 98, Appl
c 515	28.4	3.2	4929	4	US-09-874-923-98	Sequence 98, Appl
c 516	28.4	3.2	5134	4	US-09-853-450-46	Sequence 46, Appl
517	28.4	3.2	6644	4	US-08-875-435B-5	Sequence 5, Appli
518	28.4	3.2	7060	4	US-09-949-016-13337	Sequence 13337, A
c 519	28.4	3.2	10698	4	US-09-949-016-12780	Sequence 12780, A
c 520	28.4	3.2	13637	4	US-09-902-540-1097	Sequence 1097, Ap
c 521	28.4	3.2	16367	4	US-09-949-016-14509	Sequence 14509, A
522	28.4	3.2	17896	4	US-09-949-016-16867	Sequence 16867, A
c 523	28.4	3.2	18079	4	US-09-949-016-13344	Sequence 13344, A
524	28.4	3.2	20840	4	US-09-949-016-14115	Sequence 14115, A
525	28.4	3.2	36851	4	US-09-949-016-14674	Sequence 14674, A
c 526	28.4	3.2	41062	4	US-09-949-016-12761	Sequence 12761, A
c 527	28.4	3.2	41062	4	US-09-949-016-16796	Sequence 16796, A
528	28.4	3.2	50836	4	US-09-949-016-16722	Sequence 16722, A
c 529	28.4	3.2	58273	4	US-09-949-016-14679	Sequence 14679, A
530	28.4	3.2	70947	4	US-09-949-016-15165	Sequence 15165, A
531	28.4	3.2	72128	4	US-09-949-016-16018	Sequence 16018, A
532	28.4	3.2	87562	4	US-09-949-016-13685	Sequence 13685, A
533	28.4	3.2	112465	4	US-09-949-016-16424	Sequence 16424, A
c 534	28.4	3.2	112874	4	US-09-949-016-13180	Sequence 13180, A
535	28.4	3.2	125188	4	US-09-949-016-11980	Sequence 11980, A
536	28.4	3.2	134987	4	US-09-949-016-15348	Sequence 15348, A
537	28.4	3.2	134987	4	US-09-949-016-15349	Sequence 15349, A
538	28.4	3.2	134987	4	US-09-949-016-15350	Sequence 15350, A

	539	28.4	3.2	134987	4	US-09-949-016-15507	Sequence 15507, A
	540	28.4	3.2	134987	4	US-09-949-016-15508	Sequence 15508, A
	541	28.4	3.2	134987	4	US-09-949-016-15509	Sequence 15509, A
	542	28.4	3.2	187848	4	US-09-949-016-12111	Sequence 12111, A
	543	28.4	3.2	209210	4	US-09-949-016-15094	Sequence 15094, A
	544	28.4	3.2	260286	4	US-09-949-016-17037	Sequence 17037, A
	545	28.4	3.2	260293	4	US-09-949-016-12106	Sequence 12106, A
	546	28.4	3.2	536165	4	US-09-214-808-1	Sequence 1, Appli
	547	28.2	3.2	503	4	US-09-621-976-3056	Sequence 3056, Ap
c	548	28.2	3.2	601	4	US-09-949-016-45044	Sequence 45044, A
c	549	28.2	3.2	601	4	US-09-949-016-45046	Sequence 45046, A
c	550	28.2	3.2	601	4	US-09-949-016-45048	Sequence 45048, A
c	551	28.2	3.2	601	4	US-09-949-016-58730	Sequence 58730, A
c	552	28.2	3.2	601	4	US-09-949-016-87890	Sequence 87890, A
c	553	28.2	3.2	601	4	US-09-949-016-148779	Sequence 148779,
c	554	28.2	3.2	601	4	US-09-949-016-166951	Sequence 166951,
c	555	28.2	3.2	601	4	US-09-949-016-166971	Sequence 166971,
	556	28.2	3.2	730	4	US-09-328-475C-269	Sequence 269, App
	557	28.2	3.2	732	4	US-09-252-991A-11347	Sequence 11347, A
	558	28.2	3.2	745	4	US-09-328-475C-268	Sequence 268, App
c	559	28.2	3.2	807	4	US-09-252-991A-11320	Sequence 11320, A
	560	28.2	3.2	901	4	US-09-270-767-30448	Sequence 30448, A
	561	28.2	3.2	945	4	US-09-252-991A-3029	Sequence 3029, Ap
	562	28.2	3.2	1059	4	US-09-902-540-6686	Sequence 6686, Ap
c	563	28.2	3.2	1071	4	US-09-902-540-4608	Sequence 4608, Ap
	564	28.2	3.2	1188	4	US-09-949-016-2371	Sequence 2371, Ap
	565	28.2	3.2	2064	4	US-09-270-767-14306	Sequence 14306, A
	566	28.2	3.2	2289	4	US-09-252-991A-12852	Sequence 12852, A
	567	28.2	3.2	2450	4	US-09-618-425-4	Sequence 4, Appli
c	568	28.2	3.2	2725	4	US-09-902-540-527	Sequence 527, App
	569	28.2	3.2	3647	4	US-09-949-016-4704	Sequence 4704, Ap
c	570	28.2	3.2	5113	3	US-08-973-273-2	Sequence 2, Appli
c	571	28.2	3.2	5948	4	US-09-949-016-12734	Sequence 12734, A
c	572	28.2	3.2	6527	4	US-09-949-016-15163	Sequence 15163, A
c	573	28.2	3.2	7482	4	US-09-949-016-15564	Sequence 15564, A
c	574	28.2	3.2	12912	2	US-08-460-751-1	Sequence 1, Appli
c	575	28.2	3.2	12912	4	US-09-479-467A-1	Sequence 1, Appli
c	576	28.2	3.2	13807	3	US-09-052-469-5	Sequence 5, Appli
c	577	28.2	3.2	13807	4	US-08-422-582-5	Sequence 5, Appli
c	578	28.2	3.2	13807	4	US-09-052-262-5	Sequence 5, Appli
c	579	28.2	3.2	13941	4	US-09-799-451-341	Sequence 341, App
c	580	28.2	3.2	14060	3	US-08-658-136-4	Sequence 4, Appli
c	581	28.2	3.2	14148	3	US-09-052-469-7	Sequence 7, Appli
c	582	28.2	3.2	14148	4	US-08-422-582-7	Sequence 7, Appli
c	583	28.2	3.2	14148	4	US-09-052-262-7	Sequence 7, Appli
c	584	28.2	3.2	27490	4	US-09-902-540-1227	Sequence 1227, Ap
c	585	28.2	3.2	31571	1	US-08-323-443B-1	Sequence 1, Appli
	586	28.2	3.2	32998	4	US-09-408-020-1	Sequence 1, Appli
	587	28.2	3.2	33125	4	US-09-949-016-16436	Sequence 16436, A
	588	28.2	3.2	33125	4	US-09-949-016-16437	Sequence 16437, A
	589	28.2	3.2	36075	4	US-09-949-016-16571	Sequence 16571, A
	590	28.2	3.2	36075	4	US-09-949-016-16572	Sequence 16572, A
	591	28.2	3.2	36625	4	US-09-949-016-12788	Sequence 12788, A
	592	28.2	3.2	37133	4	US-09-949-016-16569	Sequence 16569, A
	593	28.2	3.2	37133	4	US-09-949-016-16570	Sequence 16570, A
c	594	28.2	3.2	40465	4	US-09-949-016-12561	Sequence 12561, A
	595	28.2	3.2	48994	4	US-09-949-016-14091	Sequence 14091, A
	596	28.2	3.2	50563	4	US-09-949-016-15821	Sequence 15821, A
c	597	28.2	3.2	53526	3	US-08-658-136-2	Sequence 2, Appli
c	598	28.2	3.2	53577	3	US-08-658-136-1	Sequence 1, Appli
	599	28.2	3.2	69924	4	US-09-949-016-15367	Sequence 15367, A
	600	28.2	3.2	77851	4	US-09-949-016-12508	Sequence 12508, A
	601	28.2	3.2	77867	4	US-09-949-016-13211	Sequence 13211, A
	602	28.2	3.2	77867	4	US-09-949-016-13212	Sequence 13212, A
	603	28.2	3.2	77940	4	US-09-949-016-12509	Sequence 12509, A
c	604	28.2	3.2	101951	4	US-09-949-016-15648	Sequence 15648, A
	605	28.2	3.2	141115	4	US-09-949-016-17490	Sequence 17490, A
c	606	28.2	3.2	163022	4	US-09-949-016-16515	Sequence 16515, A
c	607	28.2	3.2	165651	4	US-09-949-016-13032	Sequence 13032, A
c	608	28.2	3.2	172677	4	US-09-949-016-13444	Sequence 13444, A
	609	28.2	3.2	196714	4	US-09-949-016-15474	Sequence 15474, A
c	610	28.2	3.2	234884	4	US-09-949-016-16420	Sequence 16420, A
c	611	28.2	3.2	254405	4	US-09-949-016-14381	Sequence 14381, A
c	612	28	3.1	203	4	US-09-513-999C-13205	Sequence 13205, A
c	613	28	3.1	261	4	US-09-313-294A-2337	Sequence 2337, Ap
c	614	28	3.1	263	4	US-09-313-294A-3977	Sequence 3977, Ap
	615	28	3.1	295	4	US-09-313-294A-6880	Sequence 6880, Ap
	616	28	3.1	345	4	US-09-902-540-5501	Sequence 5501, Ap
	617	28	3.1	405	4	US-09-855-288-8	Sequence 8, Appli
c	618	28	3.1	473	4	US-09-513-999C-26008	Sequence 26008, A
	619	28	3.1	505	4	US-09-621-976-15639	Sequence 15639, A
	620	28	3.1	601	4	US-09-949-016-78896	Sequence 78896, A
	621	28	3.1	601	4	US-09-949-016-78897	Sequence 78897, A
c	622	28	3.1	601	4	US-09-949-016-96377	Sequence 96377, A
c	623	28	3.1	601	4	US-09-949-016-96643	Sequence 96643, A
c	624	28	3.1	601	4	US-09-949-016-96909	Sequence 96909, A
c	625	28	3.1	601	4	US-09-949-016-97175	Sequence 97175, A
c	626	28	3.1	601	4	US-09-949-016-97441	Sequence 97441, A
c	627	28	3.1	601	4	US-09-949-016-97707	Sequence 97707, A
c	628	28	3.1	601	4	US-09-949-016-97973	Sequence 97973, A
c	629	28	3.1	601	4	US-09-949-016-98239	Sequence 98239, A
c	630	28	3.1	601	4	US-09-949-016-98505	Sequence 98505, A
c	631	28	3.1	601	4	US-09-949-016-98771	Sequence 98771, A
c	632	28	3.1	601	4	US-09-949-016-99037	Sequence 99037, A
c	633	28	3.1	601	4	US-09-949-016-99303	Sequence 99303, A
c	634	28	3.1	601	4	US-09-949-016-99569	Sequence 99569, A
c	635	28	3.1	601	4	US-09-949-016-99835	Sequence 99835, A
c	636	28	3.1	601	4	US-09-949-016-100101	Sequence 100101,
c	637	28	3.1	601	4	US-09-949-016-100367	Sequence 100367,
c	638	28	3.1	601	4	US-09-949-016-100633	Sequence 100633,
c	639	28	3.1	601	4	US-09-949-016-100937	Sequence 100937,
c	640	28	3.1	601	4	US-09-949-016-101203	Sequence 101203,
c	641	28	3.1	601	4	US-09-949-016-101469	Sequence 101469,
c	642	28	3.1	601	4	US-09-949-016-101735	Sequence 101735,
	643	28	3.1	601	4	US-09-949-016-131097	Sequence 131097,
c	644	28	3.1	601	4	US-09-949-016-136523	Sequence 136523,
c	645	28	3.1	601	4	US-09-949-016-136524	Sequence 136524,
c	646	28	3.1	601	4	US-09-949-016-178700	Sequence 178700,
	647	28	3.1	601	4	US-09-949-016-199260	Sequence 199260,
	648	28	3.1	603	4	US-09-252-991A-3153	Sequence 3153, Ap
	649	28	3.1	731	4	US-09-270-767-26097	Sequence 26097, A
c	650	28	3.1	834	4	US-09-495-050A-288	Sequence 288, App
	651	28	3.1	936	4	US-09-583-110-1834	Sequence 1834, Ap
	652	28	3.1	1029	4	US-09-799-451-225	Sequence 225, App
	653	28	3.1	1059	4	US-09-949-016-5611	Sequence 5611, Ap
	654	28	3.1	1179	4	US-09-328-352-2639	Sequence 2639, Ap
	655	28	3.1	1185	4	US-09-270-767-10653	Sequence 10653, A
c	656	28	3.1	1195	4	US-09-774-528-411	Sequence 411, App
	657	28	3.1	1209	4	US-09-252-991A-6300	Sequence 6300, Ap
c	658	28	3.1	1278	4	US-09-252-991A-6009	Sequence 6009, Ap
	659	28	3.1	1516	3	US-09-059-522-4	Sequence 4, Appli
	660	28	3.1	1516	3	US-09-382-027-4	Sequence 4, Appli
c	661	28	3.1	1720	4	US-09-919-932A-1	Sequence 1, Appli
	662	28	3.1	1756	4	US-09-774-528-340	Sequence 340, App
	663	28	3.1	2057	3	US-09-059-522-2	Sequence 2, Appli
	664	28	3.1	2057	3	US-09-382-027-2	Sequence 2, Appli
	665	28	3.1	2576	3	US-09-265-108-1	Sequence 1, Appli
	666	28	3.1	2576	3	US-09-479-264-1	Sequence 1, Appli
	667	28	3.1	2628	3	US-09-294-531B-5	Sequence 5, Appli
	668	28	3.1	3469	4	US-09-560-385A-23	Sequence 23, Appl
	669	28	3.1	3511	4	US-09-560-385A-19	Sequence 19, Appl
	670	28	3.1	3585	4	US-09-560-385A-21	Sequence 21, Appl
	671	28	3.1	3621	4	US-09-560-385A-17	Sequence 17, Appl
	672	28	3.1	3759	4	US-09-560-385A-15	Sequence 15, Appl
	673	28	3.1	3804	4	US-08-999-689A-1	Sequence 1, Appli
	674	28	3.1	3930	4	US-09-560-385A-13	Sequence 13, Appl
	675	28	3.1	3931	1	US-08-144-121-1	Sequence 1, Appli
	676	28	3.1	3931	2	US-08-735-893-1	Sequence 1, Appli
	677	28	3.1	3971	4	US-09-876-176-1	Sequence 1, Appli
	678	28	3.1	4108	4	US-09-919-172-15	Sequence 15, Appl
	679	28	3.1	4267	3	US-09-661-753-47	Sequence 47, Appl
	680	28	3.1	5396	4	US-09-270-767-29115	Sequence 29115, A
c	681	28	3.1	5674	1	US-07-807-043B-8	Sequence 8, Appli
c	682	28	3.1	5674	1	US-08-190-411A-1	Sequence 1, Appli
c	683	28	3.1	5674	1	US-08-299-849B-8	Sequence 8, Appli
c	684	28	3.1	5674	2	US-08-560-024-1	Sequence 1, Appli

c 685	28	3.1	5674	2	US-08-142-368A-8	Sequence 8, Appli
c 686	28	3.1	5674	3	US-08-967-727-8	Sequence 8, Appli
c 687	28	3.1	5674	3	US-08-037-230D-8	Sequence 8, Appli
c 688	28	3.1	5674	4	US-09-583-850-8	Sequence 8, Appli
c 689	28	3.1	5674	4	US-09-579-197-8	Sequence 8, Appli
c 690	28	3.1	5674	4	US-09-404-026-8	Sequence 8, Appli
c 691	28	3.1	5674	4	US-09-312-464-8	Sequence 8, Appli
692	28	3.1	6344	3	US-08-843-417-1	Sequence 1, Appli
693	28	3.1	6344	4	US-09-527-013-1	Sequence 1, Appli
c 694	28	3.1	7011	3	US-09-268-163-9	Sequence 9, Appli
695	28	3.1	7233	4	US-09-270-767-13200	Sequence 13200, A
696	28	3.1	8517	3	US-08-827-208-1	Sequence 1, Appli
697	28	3.1	8517	3	US-09-500-358-1	Sequence 1, Appli
698	28	3.1	8517	3	US-09-498-809-1	Sequence 1, Appli
699	28	3.1	8815	4	US-09-687-731-12	Sequence 12, Appl
700	28	3.1	11254	4	US-09-902-540-1040	Sequence 1040, Ap
701	28	3.1	14712	4	US-09-949-016-15840	Sequence 15840, A
c 702	28	3.1	17318	4	US-09-949-016-13817	Sequence 13817, A
703	28	3.1	22823	4	US-09-949-016-14121	Sequence 14121, A
704	28	3.1	23995	4	US-09-949-016-17363	Sequence 17363, A
705	28	3.1	26684	4	US-09-949-016-15109	Sequence 15109, A
706	28	3.1	26684	4	US-09-949-016-15110	Sequence 15110, A
707	28	3.1	26684	4	US-09-949-016-17409	Sequence 17409, A
708	28	3.1	26684	4	US-09-949-016-17410	Sequence 17410, A
709	28	3.1	32654	4	US-09-801-191A-3	Sequence 3, Appli
710	28	3.1	32654	4	US-10-345-198-3	Sequence 3, Appli
711	28	3.1	37861	4	US-09-949-016-16872	Sequence 16872, A
c 712	28	3.1	39154	4	US-09-949-016-12384	Sequence 12384, A
c 713	28	3.1	39154	4	US-09-949-016-12801	Sequence 12801, A
c 714	28	3.1	39443	4	US-09-949-016-14326	Sequence 14326, A
c 715	28	3.1	39443	4	US-09-949-016-14327	Sequence 14327, A
716	28	3.1	51671	4	US-09-949-016-12068	Sequence 12068, A
717	28	3.1	51671	4	US-09-949-016-15962	Sequence 15962, A
718	28	3.1	51928	4	US-09-949-016-13184	Sequence 13184, A
c 719	28	3.1	64024	4	US-09-949-016-17593	Sequence 17593, A
c 720	28	3.1	71863	4	US-09-949-016-15112	Sequence 15112, A
c 721	28	3.1	89210	4	US-09-949-016-16988	Sequence 16988, A
c 722	28	3.1	97423	4	US-09-949-016-12742	Sequence 12742, A
c 723	28	3.1	97424	4	US-09-949-016-15576	Sequence 15576, A
724	28	3.1	98701	4	US-09-949-016-15898	Sequence 15898, A
725	28	3.1	98701	4	US-09-949-016-15899	Sequence 15899, A
c 726	28	3.1	106380	4	US-09-949-016-17553	Sequence 17553, A
c 727	28	3.1	121982	4	US-09-949-016-12085	Sequence 12085, A
c 728	28	3.1	121982	4	US-09-949-016-14105	Sequence 14105, A
729	28	3.1	129380	4	US-09-949-016-12544	Sequence 12544, A
c 730	28	3.1	136917	4	US-09-949-016-16369	Sequence 16369, A
c 731	28	3.1	199945	4	US-09-949-016-15436	Sequence 15436, A
732	28	3.1	222452	4	US-09-949-016-12968	Sequence 12968, A
c 733	28	3.1	275110	4	US-09-949-016-12706	Sequence 12706, A
c 734	28	3.1	275110	4	US-09-949-016-16070	Sequence 16070, A
735	28	3.1	374159	4	US-09-949-016-15868	Sequence 15868, A
736	28	3.1	784019	4	US-09-949-016-14033	Sequence 14033, A
737	28	3.1	828152	4	US-09-949-016-12777	Sequence 12777, A
738	27.8	3.1	225	4	US-09-489-039A-7030	Sequence 7030, Ap
c 739	27.8	3.1	338	4	US-09-621-976-2886	Sequence 2886, Ap
740	27.8	3.1	519	4	US-09-252-991A-14674	Sequence 14674, A
c 741	27.8	3.1	601	4	US-09-949-016-45045	Sequence 45045, A
c 742	27.8	3.1	601	4	US-09-949-016-45047	Sequence 45047, A
c 743	27.8	3.1	601	4	US-09-949-016-54048	Sequence 54048, A
744	27.8	3.1	601	4	US-09-949-016-107474	Sequence 107474,
745	27.8	3.1	601	4	US-09-949-016-107543	Sequence 107543,
c 746	27.8	3.1	601	4	US-09-949-016-108682	Sequence 108682,
c 747	27.8	3.1	601	4	US-09-949-016-143905	Sequence 143905,
c 748	27.8	3.1	601	4	US-09-949-016-143906	Sequence 143906,
c 749	27.8	3.1	601	4	US-09-949-016-152907	Sequence 152907,
750	27.8	3.1	612	4	US-09-252-991A-14359	Sequence 14359, A
751	27.8	3.1	668	4	US-09-492-308A-17	Sequence 17, Appl
752	27.8	3.1	675	4	US-09-489-039A-7093	Sequence 7093, Ap
c 753	27.8	3.1	711	2	US-08-855-261A-2	Sequence 2, Appli
c 754	27.8	3.1	711	3	US-09-227-224-2	Sequence 2, Appli
c 755	27.8	3.1	711	4	US-09-855-288-2	Sequence 2, Appli
c 756	27.8	3.1	718	4	US-09-949-016-4066	Sequence 4066, Ap
757	27.8	3.1	786	4	US-09-902-540-5264	Sequence 5264, Ap
758	27.8	3.1	878	4	US-09-774-639-35	Sequence 35, Appl
c 759	27.8	3.1	918	4	US-09-252-991A-14261	Sequence 14261, A
c 760	27.8	3.1	968	3	US-09-227-357-93	Sequence 93, Appl
761	27.8	3.1	990	2	US-08-806-959-1	Sequence 1, Appli
762	27.8	3.1	1095	4	US-09-902-540-3906	Sequence 3906, Ap
763	27.8	3.1	1206	3	US-09-153-599A-2	Sequence 2, Appli
c 764	27.8	3.1	1605	4	US-09-949-016-4001	Sequence 4001, Ap
765	27.8	3.1	1657	4	US-09-270-767-9840	Sequence 9840, Ap
c 766	27.8	3.1	1782	1	US-08-374-155A-13	Sequence 13, Appl
c 767	27.8	3.1	1782	2	US-08-785-396-13	Sequence 13, Appl
768	27.8	3.1	2283	4	US-09-949-016-4804	Sequence 4804, Ap
769	27.8	3.1	2299	3	US-09-153-599A-1	Sequence 1, Appli
770	27.8	3.1	3359	4	US-09-023-655-1229	Sequence 1229, Ap
c 771	27.8	3.1	4599	4	US-09-302-626B-61	Sequence 61, Appl
c 772	27.8	3.1	6060	1	US-07-551-531-1	Sequence 1, Appli
773	27.8	3.1	6553	4	US-09-799-451-581	Sequence 581, App
c 774	27.8	3.1	8937	2	US-08-449-933-1	Sequence 1, Appli
c 775	27.8	3.1	8937	3	US-07-966-049A-1	Sequence 1, Appli
776	27.8	3.1	9848	3	US-09-385-222A-3	Sequence 3, Appli
c 777	27.8	3.1	10706	1	US-08-411-389-1	Sequence 1, Appli
778	27.8	3.1	13027	4	US-09-949-016-14986	Sequence 14986, A
779	27.8	3.1	13347	4	US-09-949-016-14987	Sequence 14987, A
c 780	27.8	3.1	14634	4	US-09-949-016-17384	Sequence 17384, A
c 781	27.8	3.1	15330	4	US-09-949-016-15808	Sequence 15808, A
782	27.8	3.1	21375	4	US-09-902-540-1193	Sequence 1193, Ap
c 783	27.8	3.1	25431	4	US-09-949-016-13234	Sequence 13234, A
784	27.8	3.1	25882	4	US-09-949-016-14390	Sequence 14390, A
785	27.8	3.1	25882	4	US-09-949-016-14391	Sequence 14391, A
786	27.8	3.1	30783	4	US-09-902-540-1258	Sequence 1258, Ap
c 787	27.8	3.1	30820	4	US-09-949-016-17145	Sequence 17145, A
788	27.8	3.1	32379	4	US-09-949-016-15217	Sequence 15217, A
789	27.8	3.1	32379	4	US-09-949-016-15218	Sequence 15218, A
790	27.8	3.1	32379	4	US-09-949-016-15219	Sequence 15219, A
791	27.8	3.1	32379	4	US-09-949-016-15220	Sequence 15220, A
792	27.8	3.1	32379	4	US-09-949-016-15221	Sequence 15221, A
793	27.8	3.1	32379	4	US-09-949-016-15222	Sequence 15222, A
794	27.8	3.1	32379	4	US-09-949-016-15223	Sequence 15223, A
795	27.8	3.1	32379	4	US-09-949-016-15224	Sequence 15224, A
796	27.8	3.1	32379	4	US-09-949-016-15225	Sequence 15225, A
797	27.8	3.1	32379	4	US-09-949-016-15226	Sequence 15226, A
c 798	27.8	3.1	63319	4	US-09-949-016-16579	Sequence 16579, A
799	27.8	3.1	64190	4	US-09-949-016-14712	Sequence 14712, A
800	27.8	3.1	64190	4	US-09-949-016-14713	Sequence 14713, A
801	27.8	3.1	64377	4	US-09-949-016-15212	Sequence 15212, A
802	27.8	3.1	64377	4	US-09-949-016-15213	Sequence 15213, A
803	27.8	3.1	64377	4	US-09-949-016-15214	Sequence 15214, A
804	27.8	3.1	64377	4	US-09-949-016-15215	Sequence 15215, A
805	27.8	3.1	64377	4	US-09-949-016-15216	Sequence 15216, A
c 806	27.8	3.1	76563	4	US-09-949-016-17099	Sequence 17099, A
c 807	27.8	3.1	78269	4	US-09-949-016-12497	Sequence 12497, A
c 808	27.8	3.1	104520	4	US-09-949-016-13303	Sequence 13303, A
c 809	27.8	3.1	118143	4	US-09-949-016-17196	Sequence 17196, A
c 810	27.8	3.1	126029	4	US-09-949-016-14731	Sequence 14731, A
c 811	27.8	3.1	166698	4	US-09-949-016-16038	Sequence 16038, A
812	27.8	3.1	239527	4	US-09-949-016-15980	Sequence 15980, A
c 813	27.8	3.1	254964	4	US-09-949-016-12583	Sequence 12583, A
c 814	27.8	3.1	254964	4	US-09-949-016-17392	Sequence 17392, A
c 815	27.8	3.1	481115	4	US-09-949-016-11940	Sequence 11940, A
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817	27.6	3.1	360	2	US-08-997-080-79	Sequence 79, Appl
818	27.6	3.1	360	2	US-08-997-362-79	Sequence 79, Appl
819	27.6	3.1	360	3	US-08-873-970-79	Sequence 79, Appl
820	27.6	3.1	360	3	US-09-095-855-79	Sequence 79, Appl
821	27.6	3.1	360	3	US-09-324-542-79	Sequence 79, Appl
822	27.6	3.1	360	3	US-09-205-426-79	Sequence 79, Appl
c 823	27.6	3.1	410	4	US-09-621-976-50	Sequence 50, Appl
c 824	27.6	3.1	423	4	US-09-270-767-3781	Sequence 3781, Ap
c 825	27.6	3.1	423	4	US-09-270-767-19063	Sequence 19063, A
c 826	27.6	3.1	480	4	US-09-621-976-220	Sequence 220, App
c 827	27.6	3.1	537	4	US-09-252-991A-13469	Sequence 13469, A
828	27.6	3.1	601	4	US-09-949-016-30429	Sequence 30429, A
829	27.6	3.1	601	4	US-09-949-016-38649	Sequence 38649, A
830	27.6	3.1	601	4	US-09-949-016-46088	Sequence 46088, A

	831	27.6	3.1	601	4	US-09-949-016-52873	Sequence 52873, A
c	832	27.6	3.1	601	4	US-09-949-016-79687	Sequence 79687, A
	833	27.6	3.1	601	4	US-09-949-016-90144	Sequence 90144, A
	834	27.6	3.1	601	4	US-09-949-016-90170	Sequence 90170, A
	835	27.6	3.1	601	4	US-09-949-016-107775	Sequence 107775,
	836	27.6	3.1	601	4	US-09-949-016-107776	Sequence 107776,
	837	27.6	3.1	601	4	US-09-949-016-125916	Sequence 125916,
	838	27.6	3.1	601	4	US-09-949-016-136748	Sequence 136748,
	839	27.6	3.1	601	4	US-09-949-016-136749	Sequence 136749,
	840	27.6	3.1	601	4	US-09-949-016-148093	Sequence 148093,
	841	27.6	3.1	601	4	US-09-949-016-148199	Sequence 148199,
c	842	27.6	3.1	601	4	US-09-949-016-160805	Sequence 160805,
c	843	27.6	3.1	705	4	US-09-252-991A-14236	Sequence 14236, A
	844	27.6	3.1	706	4	US-09-976-594-802	Sequence 802, App
c	845	27.6	3.1	806	4	US-09-774-528-427	Sequence 427, App
	846	27.6	3.1	819	4	US-09-252-991A-11281	Sequence 11281, A
c	847	27.6	3.1	834	4	US-09-621-976-2574	Sequence 2574, Ap
c	848	27.6	3.1	846	4	US-09-252-991A-13245	Sequence 13245, A
c	849	27.6	3.1	867	4	US-09-902-540-4504	Sequence 4504, Ap
	850	27.6	3.1	879	4	US-09-252-991A-12714	Sequence 12714, A
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c	852	27.6	3.1	930	4	US-09-252-991A-4633	Sequence 4633, Ap
	853	27.6	3.1	1059	4	US-09-252-991A-7911	Sequence 7911, Ap
c	854	27.6	3.1	1122	4	US-09-252-991A-7974	Sequence 7974, Ap
	855	27.6	3.1	1134	4	US-09-252-991A-8176	Sequence 8176, Ap
	856	27.6	3.1	1150	2	US-08-989-286-2	Sequence 2, Appli
	857	27.6	3.1	1179	4	US-09-252-991A-4241	Sequence 4241, Ap
	858	27.6	3.1	1215	4	US-09-252-991A-9259	Sequence 9259, Ap
	859	27.6	3.1	1338	4	US-09-252-991A-7764	Sequence 7764, Ap
c	860	27.6	3.1	1347	4	US-09-252-991A-13659	Sequence 13659, A
c	861	27.6	3.1	1383	4	US-09-489-039A-1795	Sequence 1795, Ap
c	862	27.6	3.1	1428	4	US-09-252-991A-12923	Sequence 12923, A
c	863	27.6	3.1	1436	3	US-09-199-637A-131	Sequence 131, App
	864	27.6	3.1	1455	4	US-09-252-991A-12561	Sequence 12561, A
	865	27.6	3.1	1455	4	US-09-489-039A-175	Sequence 175, App
c	866	27.6	3.1	1488	4	US-09-252-991A-9307	Sequence 9307, Ap
c	867	27.6	3.1	1494	4	US-09-252-991A-7568	Sequence 7568, Ap
c	868	27.6	3.1	1512	4	US-09-489-039A-3551	Sequence 3551, Ap
	869	27.6	3.1	1602	4	US-09-252-991A-9270	Sequence 9270, Ap
	870	27.6	3.1	1679	4	US-09-620-312D-997	Sequence 997, App
c	871	27.6	3.1	1719	4	US-09-252-991A-4534	Sequence 4534, Ap
c	872	27.6	3.1	1803	4	US-09-252-991A-15466	Sequence 15466, A
	873	27.6	3.1	2376	4	US-09-252-991A-15323	Sequence 15323, A
	874	27.6	3.1	2401	3	US-09-320-878-20	Sequence 20, Appl
	875	27.6	3.1	2401	4	US-09-141-908-9	Sequence 9, Appli
	876	27.6	3.1	2401	4	US-09-657-440-20	Sequence 20, Appl
	877	27.6	3.1	2406	4	US-09-252-991A-11299	Sequence 11299, A
	878	27.6	3.1	2497	4	US-09-620-312D-47	Sequence 47, Appl
	879	27.6	3.1	2676	4	US-09-252-991A-15370	Sequence 15370, A
	880	27.6	3.1	2885	4	US-09-016-434-1143	Sequence 1143, Ap
	881	27.6	3.1	2909	4	US-09-949-016-1624	Sequence 1624, Ap
	882	27.6	3.1	2909	4	US-09-949-016-1625	Sequence 1625, Ap
	883	27.6	3.1	2909	4	US-09-949-016-1626	Sequence 1626, Ap
	884	27.6	3.1	2909	4	US-09-949-016-1627	Sequence 1627, Ap
	885	27.6	3.1	2976	4	US-09-774-528-317	Sequence 317, App
	886	27.6	3.1	3510	4	US-09-265-585C-95	Sequence 95, Appl
	887	27.6	3.1	10480	4	US-09-732-615-13	Sequence 13, Appl
	888	27.6	3.1	10480	4	US-10-273-051-13	Sequence 13, Appl
c	889	27.6	3.1	15108	4	US-09-949-016-11786	Sequence 11786, A
c	890	27.6	3.1	15108	4	US-09-949-016-17205	Sequence 17205, A
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c	892	27.6	3.1	15872	4	US-09-091-609-1	Sequence 1, Appli
c	893	27.6	3.1	15872	4	US-09-091-609-3	Sequence 3, Appli
	894	27.6	3.1	16047	4	US-09-949-016-16510	Sequence 16510, A
	895	27.6	3.1	16047	4	US-09-949-016-16511	Sequence 16511, A
	896	27.6	3.1	16600	4	US-09-949-016-13332	Sequence 13332, A
	897	27.6	3.1	16600	4	US-09-949-016-13333	Sequence 13333, A
	898	27.6	3.1	21535	4	US-09-949-016-12826	Sequence 12826, A
	899	27.6	3.1	21535	4	US-09-949-016-12827	Sequence 12827, A
	900	27.6	3.1	21535	4	US-09-949-016-12828	Sequence 12828, A
	901	27.6	3.1	21535	4	US-09-949-016-12829	Sequence 12829, A
	902	27.6	3.1	21536	4	US-09-949-016-13366	Sequence 13366, A
	903	27.6	3.1	21536	4	US-09-949-016-13367	Sequence 13367, A
	904	27.6	3.1	21536	4	US-09-949-016-13368	Sequence 13368, A
	905	27.6	3.1	21536	4	US-09-949-016-13369	Sequence 13369, A
	906	27.6	3.1	25370	4	US-09-949-016-12109	Sequence 12109, A
	907	27.6	3.1	25375	4	US-09-949-016-15880	Sequence 15880, A
	908	27.6	3.1	26086	4	US-09-949-016-15355	Sequence 15355, A
	909	27.6	3.1	26238	4	US-09-949-016-12314	Sequence 12314, A
	910	27.6	3.1	26624	4	US-09-949-016-13269	Sequence 13269, A
	911	27.6	3.1	28320	4	US-09-902-540-1222	Sequence 1222, Ap
	912	27.6	3.1	29624	4	US-09-949-016-12367	Sequence 12367, A
	913	27.6	3.1	29624	4	US-09-949-016-13943	Sequence 13943, A
c	914	27.6	3.1	33731	4	US-09-949-016-13473	Sequence 13473, A
c	915	27.6	3.1	33731	4	US-09-949-016-13474	Sequence 13474, A
	916	27.6	3.1	36103	4	US-09-949-016-16382	Sequence 16382, A
c	917	27.6	3.1	36241	4	US-08-311-731A-134	Sequence 134, App
	918	27.6	3.1	37004	4	US-09-949-016-15317	Sequence 15317, A
c	919	27.6	3.1	38814	4	US-09-949-016-13470	Sequence 13470, A
c	920	27.6	3.1	38814	4	US-09-949-016-13471	Sequence 13471, A
	921	27.6	3.1	44244	4	US-09-949-016-11743	Sequence 11743, A
	922	27.6	3.1	44245	4	US-09-949-016-13579	Sequence 13579, A
	923	27.6	3.1	45427	4	US-09-949-016-16243	Sequence 16243, A
	924	27.6	3.1	45840	4	US-09-949-016-13903	Sequence 13903, A
	925	27.6	3.1	45840	4	US-09-949-016-15042	Sequence 15042, A
	926	27.6	3.1	46559	4	US-09-949-016-15043	Sequence 15043, A
	927	27.6	3.1	53394	4	US-09-949-016-15817	Sequence 15817, A
	928	27.6	3.1	53394	4	US-09-949-016-15818	Sequence 15818, A
	929	27.6	3.1	53394	4	US-09-949-016-15819	Sequence 15819, A
	930	27.6	3.1	53394	4	US-09-949-016-15820	Sequence 15820, A
	931	27.6	3.1	57859	4	US-09-949-016-12334	Sequence 12334, A
	932	27.6	3.1	57859	4	US-09-949-016-14657	Sequence 14657, A
	933	27.6	3.1	57859	4	US-09-949-016-14658	Sequence 14658, A
	934	27.6	3.1	86639	4	US-09-949-016-17397	Sequence 17397, A
	935	27.6	3.1	95122	4	US-09-949-016-17235	Sequence 17235, A
	936	27.6	3.1	152132	4	US-09-949-016-13845	Sequence 13845, A
	937	27.6	3.1	152145	4	US-09-949-016-12371	Sequence 12371, A
c	938	27.6	3.1	162914	4	US-09-949-016-15578	Sequence 15578, A
c	939	27.6	3.1	169334	4	US-09-949-016-15999	Sequence 15999, A
c	940	27.6	3.1	389504	4	US-09-949-016-11774	Sequence 11774, A
c	941	27.6	3.1	390890	4	US-09-949-016-14720	Sequence 14720, A
c	942	27.6	3.1	455726	4	US-09-949-016-14157	Sequence 14157, A
c	943	27.6	3.1	536165	4	US-09-214-808-1	Sequence 1, Appli
	944	27.4	3.1	300	3	US-09-172-108-2	Sequence 2, Appli
	945	27.4	3.1	300	3	US-09-172-711-3	Sequence 3, Appli
	946	27.4	3.1	313	4	US-09-023-655-837	Sequence 837, App
	947	27.4	3.1	344	3	US-09-615-192A-243	Sequence 243, App
	948	27.4	3.1	463	1	US-08-253-155A-59	Sequence 59, Appl
c	949	27.4	3.1	534	3	US-08-833-167-87	Sequence 87, Appl
c	950	27.4	3.1	534	3	US-09-344-837A-87	Sequence 87, Appl
	951	27.4	3.1	577	4	US-09-621-976-15251	Sequence 15251, A
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	953	27.4	3.1	601	4	US-09-949-016-34126	Sequence 34126, A
	954	27.4	3.1	601	4	US-09-949-016-41830	Sequence 41830, A
	955	27.4	3.1	601	4	US-09-949-016-58688	Sequence 58688, A
	956	27.4	3.1	601	4	US-09-949-016-58689	Sequence 58689, A
	957	27.4	3.1	601	4	US-09-949-016-60445	Sequence 60445, A
	958	27.4	3.1	601	4	US-09-949-016-69577	Sequence 69577, A
c	959	27.4	3.1	601	4	US-09-949-016-78768	Sequence 78768, A
c	960	27.4	3.1	601	4	US-09-949-016-87887	Sequence 87887, A
c	961	27.4	3.1	601	4	US-09-949-016-87888	Sequence 87888, A
c	962	27.4	3.1	601	4	US-09-949-016-112372	Sequence 112372,
c	963	27.4	3.1	601	4	US-09-949-016-112373	Sequence 112373,
	964	27.4	3.1	601	4	US-09-949-016-132813	Sequence 132813,
	965	27.4	3.1	601	4	US-09-949-016-132814	Sequence 132814,
	966	27.4	3.1	601	4	US-09-949-016-132815	Sequence 132815,
c	967	27.4	3.1	601	4	US-09-949-016-162087	Sequence 162087,
	968	27.4	3.1	601	4	US-09-949-016-169910	Sequence 169910,
	969	27.4	3.1	601	4	US-09-949-016-175256	Sequence 175256,
	970	27.4	3.1	601	4	US-09-949-016-175258	Sequence 175258,
c	971	27.4	3.1	601	4	US-09-949-016-188329	Sequence 188329,
c	972	27.4	3.1	601	4	US-09-949-016-188330	Sequence 188330,
	973	27.4	3.1	687	3	US-09-615-192A-242	Sequence 242, App
	974	27.4	3.1	1098	4	US-09-602-777A-405	Sequence 405, App
	975	27.4	3.1	1159	4	US-09-799-451-552	Sequence 552, App
c	976	27.4	3.1	1256	4	US-09-896-866B-6	Sequence 6, Appli

977	27.4	3.1	1266	4	US-09-902-540-3571	Sequence 3571, Ap
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c 979	27.4	3.1	1302	4	US-09-896-866B-5	Sequence 5, Appli
c 980	27.4	3.1	1308	2	US-08-404-531B-1	Sequence 1, Appli
c 981	27.4	3.1	1308	2	US-08-404-531B-2	Sequence 2, Appli
c 982	27.4	3.1	1308	3	US-08-476-900A-1	Sequence 1, Appli
c 983	27.4	3.1	1308	3	US-08-476-900A-2	Sequence 2, Appli
c 984	27.4	3.1	1308	3	US-08-488-546A-1	Sequence 1, Appli
c 985	27.4	3.1	1308	3	US-08-488-546A-2	Sequence 2, Appli
c 986	27.4	3.1	1317	4	US-09-896-866B-9	Sequence 9, Appli
987	27.4	3.1	1368	4	US-09-902-540-5949	Sequence 5949, Ap
988	27.4	3.1	1420	3	US-09-362-506-1	Sequence 1, Appli
989	27.4	3.1	1423	3	US-08-961-083-59	Sequence 59, Appl
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993	27.4	3.1	1683	4	US-09-583-110-2519	Sequence 2519, Ap
994	27.4	3.1	1692	4	US-09-107-433-1976	Sequence 1976, Ap
995	27.4	3.1	1720	4	US-09-902-540-198	Sequence 198, App
996	27.4	3.1	1790	4	US-08-997-685A-11	Sequence 11, Appl
997	27.4	3.1	1792	4	US-09-086-436-40	Sequence 40, Appl
998	27.4	3.1	2043	4	US-09-252-991A-10068	Sequence 10068, A
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c1004	27.4	3.1	2454	3	US-08-476-900A-32	Sequence 32, Appl
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1007	27.4	3.1	2571	4	US-10-277-032-1	Sequence 1, Appli
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1011	27.4	3.1	2793	4	US-09-949-016-3002	Sequence 3002, Ap
1012	27.4	3.1	2793	4	US-09-949-016-3003	Sequence 3003, Ap
1013	27.4	3.1	2793	4	US-09-949-016-3004	Sequence 3004, Ap
1014	27.4	3.1	2815	4	US-09-657-013-43	Sequence 43, Appl
c1015	27.4	3.1	2903	4	US-09-799-451-871	Sequence 871, App
c1016	27.4	3.1	2943	3	US-09-221-017B-153	Sequence 153, App
1017	27.4	3.1	2961	4	US-09-657-013-44	Sequence 44, Appl
1018	27.4	3.1	2961	4	US-09-949-016-2995	Sequence 2995, Ap
1019	27.4	3.1	2961	4	US-09-949-016-2996	Sequence 2996, Ap
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1023	27.4	3.1	2988	4	US-09-949-016-3005	Sequence 3005, Ap
1024	27.4	3.1	2988	4	US-09-949-016-3006	Sequence 3006, Ap
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1026	27.4	3.1	2988	4	US-09-949-016-3008	Sequence 3008, Ap
1027	27.4	3.1	2988	4	US-09-949-016-3009	Sequence 3009, Ap
1028	27.4	3.1	3235	4	US-09-949-016-1392	Sequence 1392, Ap
1029	27.4	3.1	3372	4	US-09-949-016-165	Sequence 165, App
1030	27.4	3.1	3650	4	US-09-949-016-5637	Sequence 5637, Ap
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1034	27.4	3.1	5655	3	US-08-996-685-1	Sequence 1, Appli
1035	27.4	3.1	5655	3	US-08-880-179-2	Sequence 2, Appli
1036	27.4	3.1	6045	3	US-08-675-566-18	Sequence 18, Appl
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1038	27.4	3.1	6447	3	US-08-675-566-16	Sequence 16, Appl
1039	27.4	3.1	6578	3	US-08-675-566-4	Sequence 4, Appli
1040	27.4	3.1	6612	3	US-08-675-566-15	Sequence 15, Appl
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1042	27.4	3.1	6994	3	US-08-675-566-1	Sequence 1, Appli
1043	27.4	3.1	7001	3	US-08-675-566-3	Sequence 3, Appli
1044	27.4	3.1	7096	3	US-09-221-017B-373	Sequence 373, App
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1049	27.4	3.1	9515	1	US-08-920-827-13	Sequence 13, Appl
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1052	27.4	3.1	9515	2	US-08-920-828-13	Sequence 13, Appl
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1055	27.4	3.1	10424	4	US-09-902-540-1015	Sequence 1015, Ap
1056	27.4	3.1	11220	3	US-09-105-537-32	Sequence 32, Appl
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1068	27.4	3.1	30006	4	US-09-949-016-16385	Sequence 16385, A
1069	27.4	3.1	31300	4	US-09-949-016-16967	Sequence 16967, A
1070	27.4	3.1	31467	4	US-09-949-016-13134	Sequence 13134, A
1071	27.4	3.1	31868	4	US-09-949-016-11907	Sequence 11907, A
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c1076	27.4	3.1	34303	3	US-09-315-372-4	Sequence 4, Appli
c1077	27.4	3.1	34303	3	US-09-244-752-4	Sequence 4, Appli
c1078	27.4	3.1	34303	3	US-09-245-497-4	Sequence 4, Appli
c1079	27.4	3.1	34303	3	US-09-562-919-4	Sequence 4, Appli
c1080	27.4	3.1	34382	2	US-08-374-483-6	Sequence 6, Appli
c1081	27.4	3.1	35408	3	US-08-973-334-3	Sequence 3, Appli
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c1085	27.4	3.1	35935	2	US-08-735-609-1	Sequence 1, Appli
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1098	27.4	3.1	38506	4	US-09-141-908-1	Sequence 1, Appli
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c1127	27.4	3.1	150409	4	US-09-949-016-12938	Sequence 12938, A
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c1129	27.4	3.1	157644	4	US-09-949-016-16180	Sequence 16180, A
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c1133	27.4	3.1	161914	4	US-09-949-016-12906	Sequence 12906, A
1134	27.4	3.1	172677	4	US-09-949-016-13444	Sequence 13444, A
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c1136	27.4	3.1	194714	4	US-09-949-016-11869	Sequence 11869, A
c1137	27.4	3.1	196714	4	US-09-949-016-15474	Sequence 15474, A
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1142	27.4	3.1	254964	4	US-09-949-016-17392	Sequence 17392, A
c1143	27.4	3.1	300402	4	US-09-949-016-13632	Sequence 13632, A
1144	27.4	3.1	323820	4	US-09-949-016-14139	Sequence 14139, A
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1155	27.2	3.1	307	4	US-09-270-767-17217	Sequence 17217, A
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1164	27.2	3.1	601	4	US-09-949-016-71222	Sequence 71222, A
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1171	27.2	3.1	601	4	US-09-949-016-103042	Sequence 103042,
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1173	27.2	3.1	601	4	US-09-949-016-103117	Sequence 103117,
1174	27.2	3.1	601	4	US-09-949-016-107777	Sequence 107777,
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1176	27.2	3.1	601	4	US-09-949-016-134862	Sequence 134862,
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1179	27.2	3.1	601	4	US-09-949-016-187928	Sequence 187928,
1180	27.2	3.1	601	4	US-09-949-016-187929	Sequence 187929,
c1181	27.2	3.1	716	3	US-08-998-416-725	Sequence 725, App
c1182	27.2	3.1	720	3	US-08-998-416-992	Sequence 992, App
c1183	27.2	3.1	747	4	US-09-252-991A-14368	Sequence 14368, A
1184	27.2	3.1	795	4	US-09-252-991A-14337	Sequence 14337, A
1185	27.2	3.1	879	4	US-09-902-540-7290	Sequence 7290, Ap
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1187	27.2	3.1	924	4	US-09-902-540-3180	Sequence 3180, Ap
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1189	27.2	3.1	1002	4	US-09-902-540-3214	Sequence 3214, Ap
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c1193	27.2	3.1	1407	4	US-09-252-991A-11113	Sequence 11113, A
c1194	27.2	3.1	1416	4	US-09-252-991A-11168	Sequence 11168, A
c1195	27.2	3.1	1502	2	US-08-805-965-6	Sequence 6, Appli
c1196	27.2	3.1	1521	4	US-09-949-016-2482	Sequence 2482, Ap
1197	27.2	3.1	1542	4	US-09-489-039A-3753	Sequence 3753, Ap
1198	27.2	3.1	1590	4	US-09-252-991A-11088	Sequence 11088, A
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c1200	27.2	3.1	1635	4	US-09-328-352-320	Sequence 320, App
c1201	27.2	3.1	1671	4	US-09-252-991A-6099	Sequence 6099, Ap
c1202	27.2	3.1	1674	4	US-09-252-991A-6179	Sequence 6179, Ap
1203	27.2	3.1	1743	4	US-09-252-991A-6372	Sequence 6372, Ap
1204	27.2	3.1	1743	4	US-09-902-540-9536	Sequence 9536, Ap
1205	27.2	3.1	1809	4	US-09-620-312D-1082	Sequence 1082, Ap
1206	27.2	3.1	1820	1	US-08-173-508-7	Sequence 7, Appli
1207	27.2	3.1	1821	2	US-08-265-310-7	Sequence 7, Appli
1208	27.2	3.1	1821	3	US-08-951-742-7	Sequence 7, Appli
1209	27.2	3.1	1848	4	US-09-902-540-7792	Sequence 7792, Ap
1210	27.2	3.1	1992	3	US-09-484-970B-150	Sequence 150, App
1211	27.2	3.1	2110	4	US-09-949-016-4488	Sequence 4488, Ap
1212	27.2	3.1	2138	4	US-09-949-016-4729	Sequence 4729, Ap
1213	27.2	3.1	2211	3	US-09-318-448-26	Sequence 26, Appl
1214	27.2	3.1	2211	3	US-09-347-878-2	Sequence 2, Appli
1215	27.2	3.1	2211	4	US-09-546-013-4	Sequence 4, Appli
1216	27.2	3.1	2238	4	US-09-489-039A-3733	Sequence 3733, Ap
1217	27.2	3.1	2463	1	US-08-339-578-1	Sequence 1, Appli
1218	27.2	3.1	2823	4	US-09-270-767-1868	Sequence 1868, Ap
1219	27.2	3.1	2823	4	US-09-270-767-17150	Sequence 17150, A
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1221	27.2	3.1	3045	4	US-09-949-016-701	Sequence 701, App
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1223	27.2	3.1	3260	2	US-08-436-900A-3	Sequence 3, Appli
1224	27.2	3.1	3536	4	US-09-949-016-1083	Sequence 1083, Ap
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c1226	27.2	3.1	4465	4	US-09-949-016-2042	Sequence 2042, Ap
1227	27.2	3.1	4978	4	US-09-902-540-775	Sequence 775, App
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1230	27.2	3.1	8078	3	US-09-445-247-12	Sequence 12, Appl
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c1233	27.2	3.1	9035	4	US-09-902-540-1084	Sequence 1084, Ap
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1235	27.2	3.1	9506	4	US-09-949-016-16449	Sequence 16449, A
c1236	27.2	3.1	11465	4	US-09-949-016-13842	Sequence 13842, A
1237	27.2	3.1	11858	4	US-09-949-016-12443	Sequence 12443, A
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c1239	27.2	3.1	11958	4	US-09-664-186-8	Sequence 8, Appli
1240	27.2	3.1	12299	4	US-09-902-540-1056	Sequence 1056, Ap
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1243	27.2	3.1	14985	5	PCT-US96-06231A-6	Sequence 6, Appli
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1248	27.2	3.1	21296	4	US-09-949-016-14505	Sequence 14505, A
1249	27.2	3.1	21296	4	US-09-949-016-15701	Sequence 15701, A
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1252	27.2	3.1	23825	4	US-09-949-016-13936	Sequence 13936, A
1253	27.2	3.1	28809	4	US-09-949-016-12825	Sequence 12825, A
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1255	27.2	3.1	39176	4	US-09-949-016-17603	Sequence 17603, A
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c1259	27.2	3.1	63183	4	US-09-949-016-13048	Sequence 13048, A
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c1264	27.2	3.1	82125	4	US-09-949-016-13518	Sequence 13518, A
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1268	27.2	3.1	100837	4	US-09-949-016-17063	Sequence 17063, A

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1271	27.2	3.1	126200	4	US-09-949-016-13193	Sequence 13193, A
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1273	27.2	3.1	146039	4	US-09-949-016-12449	Sequence 12449, A
1274	27.2	3.1	155266	4	US-09-949-016-13870	Sequence 13870, A
1275	27.2	3.1	163181	4	US-09-949-016-13730	Sequence 13730, A
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c1278	27.2	3.1	276237	4	US-09-949-016-17504	Sequence 17504, A
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1280	27.2	3.1	302604	4	US-09-949-016-14588	Sequence 14588, A
1281	27.2	3.1	302604	4	US-09-949-016-14589	Sequence 14589, A
1282	27.2	3.1	308362	4	US-09-949-016-17119	Sequence 17119, A
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1284	27.2	3.1	476044	4	US-09-949-016-12412	Sequence 12412, A
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c1286	27.2	3.1	670690	4	US-09-949-016-14207	Sequence 14207, A
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c1292	27	3.0	450	4	US-09-270-767-16534	Sequence 16534, A
1293	27	3.0	455	4	US-09-513-999C-9269	Sequence 9269, Ap
1294	27	3.0	456	4	US-09-252-991A-15624	Sequence 15624, A
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1296	27	3.0	498	4	US-09-252-991A-2063	Sequence 2063, Ap
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c1298	27	3.0	555	5	PCT-US94-12873-13	Sequence 13, Appl
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c1301	27	3.0	601	4	US-09-949-016-58140	Sequence 58140, A
1302	27	3.0	601	4	US-09-949-016-63090	Sequence 63090, A
1303	27	3.0	601	4	US-09-949-016-69578	Sequence 69578, A
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c1312	27	3.0	601	4	US-09-949-016-137561	Sequence 137561,
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1314	27	3.0	601	4	US-09-949-016-159094	Sequence 159094,
1315	27	3.0	601	4	US-09-949-016-166806	Sequence 166806,
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c1324	27	3.0	601	4	US-09-949-016-191808	Sequence 191808,
c1325	27	3.0	601	4	US-09-949-016-191986	Sequence 191986,
c1326	27	3.0	601	4	US-09-949-016-192164	Sequence 192164,
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1328	27	3.0	624	4	US-09-902-540-6267	Sequence 6267, Ap
1329	27	3.0	636	4	US-09-252-991A-4615	Sequence 4615, Ap
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1332	27	3.0	960	1	US-08-597-495B-23	Sequence 23, Appl
1333	27	3.0	960	3	US-09-068-051A-23	Sequence 23, Appl
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1335	27	3.0	1002	3	US-09-257-179-27	Sequence 27, Appl
1336	27	3.0	1083	4	US-09-252-991A-2517	Sequence 2517, Ap
1337	27	3.0	1101	3	US-08-987-904A-3	Sequence 3, Appli
1338	27	3.0	1101	4	US-09-438-623A-3	Sequence 3, Appli
1339	27	3.0	1107	4	US-09-252-991A-3881	Sequence 3881, Ap
1340	27	3.0	1113	4	US-09-489-039A-1851	Sequence 1851, Ap
1341	27	3.0	1155	4	US-09-252-991A-4515	Sequence 4515, Ap
1342	27	3.0	1161	4	US-09-679-971-1	Sequence 1, Appli
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c1344	27	3.0	1182	4	US-09-252-991A-200	Sequence 200, App
1345	27	3.0	1185	4	US-09-902-540-8425	Sequence 8425, Ap
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c1347	27	3.0	1269	4	US-09-252-991A-11061	Sequence 11061, A
1348	27	3.0	1317	4	US-09-252-991A-2139	Sequence 2139, Ap
1349	27	3.0	1337	4	US-09-270-767-14156	Sequence 14156, A
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c1353	27	3.0	1387	4	US-10-321-210-13	Sequence 13, Appl
c1354	27	3.0	1387	4	US-10-320-874-13	Sequence 13, Appl
c1355	27	3.0	1392	4	US-09-902-540-7904	Sequence 7904, Ap
1356	27	3.0	1394	3	US-09-453-702B-30	Sequence 30, Appl
c1357	27	3.0	1431	4	US-09-252-991A-2397	Sequence 2397, Ap
1358	27	3.0	1452	4	US-09-543-681A-1985	Sequence 1985, Ap
1359	27	3.0	1488	4	US-09-949-016-5480	Sequence 5480, Ap
1360	27	3.0	1577	4	US-09-949-016-5782	Sequence 5782, Ap
c1361	27	3.0	1578	4	US-09-602-787A-613	Sequence 613, App
1362	27	3.0	1641	4	US-09-252-991A-11134	Sequence 11134, A
1363	27	3.0	1656	4	US-09-902-540-3251	Sequence 3251, Ap
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1366	27	3.0	1701	4	US-09-252-991A-219	Sequence 219, App
1367	27	3.0	1938	4	US-09-252-991A-228	Sequence 228, App
1368	27	3.0	1962	2	US-08-919-421A-1	Sequence 1, Appli
1369	27	3.0	1962	3	US-09-342-819-1	Sequence 1, Appli
1370	27	3.0	1962	4	US-09-526-833-1	Sequence 1, Appli
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c1372	27	3.0	1989	4	US-09-252-991A-1821	Sequence 1821, Ap
1373	27	3.0	2012	4	US-09-561-861-1	Sequence 1, Appli
1374	27	3.0	2211	4	US-09-252-991A-15685	Sequence 15685, A
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c1376	27	3.0	2406	2	US-08-461-379A-1	Sequence 1, Appli
c1377	27	3.0	2406	2	US-08-462-390B-1	Sequence 1, Appli
c1378	27	3.0	2406	3	US-08-463-074B-1	Sequence 1, Appli
c1379	27	3.0	2406	3	US-08-465-585C-1	Sequence 1, Appli
c1380	27	3.0	2406	3	US-08-652-446-1	Sequence 1, Appli
1381	27	3.0	2415	3	US-09-306-922-1	Sequence 1, Appli
c1382	27	3.0	2453	4	US-09-902-540-429	Sequence 429, App
1383	27	3.0	2496	4	US-09-799-451-872	Sequence 872, App
c1384	27	3.0	2534	4	US-09-949-016-3864	Sequence 3864, Ap
1385	27	3.0	2565	1	US-08-597-495B-29	Sequence 29, Appl
1386	27	3.0	2565	3	US-09-068-051A-31	Sequence 31, Appl
c1387	27	3.0	2763	4	US-09-902-540-2542	Sequence 2542, Ap
1388	27	3.0	2793	3	US-09-336-536-68	Sequence 68, Appl
1389	27	3.0	2803	3	US-09-068-051A-33	Sequence 33, Appl
1390	27	3.0	2906	4	US-09-799-451-498	Sequence 498, App
1391	27	3.0	3037	4	US-09-949-016-5389	Sequence 5389, Ap
1392	27	3.0	3311	2	US-08-239-276-10	Sequence 10, Appl
1393	27	3.0	3311	2	US-08-468-579B-10	Sequence 10, Appl
1394	27	3.0	3311	3	US-08-468-577B-10	Sequence 10, Appl
1395	27	3.0	3311	4	US-08-468-581A-10	Sequence 10, Appl
1396	27	3.0	3423	4	US-09-620-312D-126	Sequence 126, App
1397	27	3.0	3613	3	US-08-514-213A-1	Sequence 1, Appli
1398	27	3.0	3613	4	US-09-015-399-9	Sequence 9, Appli
1399	27	3.0	3637	4	US-09-566-921-5	Sequence 5, Appli
1400	27	3.0	3711	4	US-09-566-921-126	Sequence 126, App
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c1403	27	3.0	5159	4	US-09-560-385A-33	Sequence 33, Appl
c1404	27	3.0	6065	4	US-09-800-729-35	Sequence 35, Appl
1405	27	3.0	6288	4	US-09-949-016-12483	Sequence 12483, A
1406	27	3.0	6553	4	US-09-902-540-885	Sequence 885, App
1407	27	3.0	7948	4	US-09-949-016-14929	Sequence 14929, A
1408	27	3.0	7950	4	US-09-949-016-14352	Sequence 14352, A
1409	27	3.0	7960	4	US-09-949-016-14930	Sequence 14930, A
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1411	27	3.0	8658	4	US-09-902-540-943	Sequence 943, App
1412	27	3.0	11500	4	US-09-949-016-13970	Sequence 13970, A
1413	27	3.0	14641	4	US-09-949-016-15834	Sequence 15834, A
1414	27	3.0	15312	4	US-09-902-540-1115	Sequence 1115, Ap

1415	27	3.0	19009	4	US-09-949-016-12522	Sequence 12522, A
1416	27	3.0	19012	4	US-09-949-016-16999	Sequence 16999, A
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1418	27	3.0	19954	4	US-09-902-540-1150	Sequence 1150, Ap
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c1420	27	3.0	22761	4	US-09-902-540-1219	Sequence 1219, Ap
1421	27	3.0	23394	4	US-09-949-016-17131	Sequence 17131, A
c1422	27	3.0	26711	4	US-09-949-016-14214	Sequence 14214, A
c1423	27	3.0	27120	4	US-09-949-016-16210	Sequence 16210, A
c1424	27	3.0	28509	4	US-09-902-540-1240	Sequence 1240, Ap
1425	27	3.0	29629	3	US-09-729-995-3	Sequence 3, Appli
1426	27	3.0	29629	4	US-10-135-689-3	Sequence 3, Appli
1427	27	3.0	29629	4	US-10-690-617-3	Sequence 3, Appli
1428	27	3.0	36899	4	US-09-949-016-13566	Sequence 13566, A
1429	27	3.0	40219	4	US-09-949-016-15337	Sequence 15337, A
1430	27	3.0	42053	4	US-09-949-016-15924	Sequence 15924, A
c1431	27	3.0	47471	4	US-09-949-016-12271	Sequence 12271, A
1432	27	3.0	47698	4	US-09-949-016-13514	Sequence 13514, A
c1433	27	3.0	54986	4	US-09-949-016-16716	Sequence 16716, A
c1434	27	3.0	56678	4	US-09-949-016-17453	Sequence 17453, A
c1435	27	3.0	58543	4	US-09-949-016-13565	Sequence 13565, A
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1444	27	3.0	80355	4	US-09-949-016-12735	Sequence 12735, A
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ALIGNMENTS

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RESULT 1
US-09-208-718-4
; Sequence 4, Application US/09208718
; Patent No. 6063767
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Hillman, Jennifer
;    APPLICANT:  Corley, Neil
;    APPLICANT:  Shah, Purvi
;    TITLE OF INVENTION:  HUMAN PHOSPHOLIPID BINDING PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,718
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/958,820
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0379 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  903 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGTUT12
;      CLONE:  3126479
US-09-208-718-4

  Query Match           96.4%;  Score 858.4;  DB 3;  Length 903;
  Best Local Similarity  99.2%;  Pred. No. 2.5e-273;
  Matches  873;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

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RESULT 2
US-09-621-976-7
; Sequence 7, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7

; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..695
; NAME/KEY: sig_peptide
; LOCATION: 15..80
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.5
; OTHER INFORMATION: seq AALLLGLMMVVTG/DE
US-09-621-976-7

Query Match 88.1%; Score 783.8; DB 4; Length 826;
Best Local Similarity 99.0%; Pred. No. 1.2e-248;
Matches 799; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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RESULT 3
US-09-513-999C-7
; Sequence 7, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 7
;   LENGTH: 826
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
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;   NAME/KEY: sig_peptide
;   LOCATION: 15..80
;   OTHER INFORMATION: score 8.5
;   OTHER INFORMATION: seq AALLLGLMMVVTG/DE
US-09-513-999C-7

  Query Match             88.1%;  Score 783.8;  DB 4;  Length 826;
  Best Local Similarity   99.0%;  Pred. No. 1.2e-248;
  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

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RESULT 4
US-09-471-276-7
; Sequence 7, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Duclert A.
;  APPLICANT: Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
;  FILE REFERENCE: GENSET.025CP1
;  CURRENT APPLICATION NUMBER: US/09/471,276
;  CURRENT FILING DATE: 1999-12-21
;  EARLIER APPLICATION NUMBER: 09/057,719
;  EARLIER FILING DATE: 1998-04-09
;  EARLIER APPLICATION NUMBER: 09/069,047
;  EARLIER FILING DATE: 1998-04-28
;  EARLIER APPLICATION NUMBER: PCT/IB99/00712
;  EARLIER FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 1622
;  SOFTWARE: Patent.pm
; SEQ ID NO 7
;   LENGTH: 826
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 15..695
;   NAME/KEY: sig_peptide
;   LOCATION: 15..80
;   OTHER INFORMATION: score 8.5
;   OTHER INFORMATION: seq AALLLGLMMVVTG/DE
US-09-471-276-7

  Query Match             88.1%;  Score 783.8;  DB 4;  Length 826;
  Best Local Similarity   99.0%;  Pred. No. 1.2e-248;
  Matches  799;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 60

Qy         135 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCT 194
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCC 120

Qy         195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 180

Qy         255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 240
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Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 300

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 360

Qy        435 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCT 420

Qy        495 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATC 480

Qy        555 TTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 614
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCAGGAAGGAAAGGTCATCTCTCTCCTTCCCAAGGAAAACAAAACTCGAGGCTCTTGGA 540

Qy        615 AAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 674
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        541 AAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCA 600

Qy        675 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGC 734
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        601 TGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGC 660

Qy        735 CCAAGCAC-AAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 793
              |||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        661 CCAAGCACAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGG 720

Qy        794 CATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 853
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGTGGCCACACTGCCCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAA 780

Qy        854 CCCCTTCTTTTCCAAATTAAAAAAAAA 880
              |||||||||||||||| |||||||||
Db        781 CCCCTTCTTTTCCAAATAAAAAAAAAA 807


RESULT 5
US-08-403-378B-3
; Sequence 3, Application US/08403378B
; Patent No. 5759991
;  GENERAL INFORMATION:
;    APPLICANT:  TOHDOH, NAOKI
;    APPLICANT:  TOJO, SHIN-ICHIRO
;    APPLICANT:  KOJIMA, SHIN-ICHI
;    APPLICANT:  UEKI, YASUYUKI
;    APPLICANT:  NISHIHARA, TOSHIO
;    APPLICANT:  FUKUSHIMA, NOBUYUKI
;    APPLICANT:  IRIE, TSUNEMASA
;    APPLICANT:  ONO, KEIICHI
;    APPLICANT:  AGUI, HIDEO
;    APPLICANT:  OJIKA, KOSEI
;    TITLE OF INVENTION:  NEUROTROPHIC PEPTIDE DERIVATIVES
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 PENNSYLVANIA AVENUE, NW
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,378B
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-124688
;      FILING DATE:  27-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-080398
;      FILING DATE:  30-MAR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-280590
;      FILING DATE:  27-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-333241
;      FILING DATE:  21-DEC-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-243003
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/758,043
;      FILING DATE:  12-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/873,764
;      FILING DATE:  27-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/01214
;      FILING DATE:  27-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BIGGART, WADDELL A
;      REGISTRATION NUMBER:  24,861
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1047 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Rattus norvegicus
;      STRAIN:  Wistar
;      TISSUE TYPE:  hippocampal tissue of brain
;    IMMEDIATE SOURCE:
;      CLONE:  A010-12
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  26..586
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..25
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  26..586
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  587..1047
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1008..1047
;    FEATURE:
;      NAME/KEY:  polyA_signal
;      LOCATION:  987..992
US-08-403-378B-3

  Query Match             5.1%;  Score 45.4;  DB 1;  Length 1047;
  Best Local Similarity   45.4%;  Pred. No. 0.00038;
  Matches  163;  Conservative    0;  Mismatches  196;  Indels    0;  Gaps    0;
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Qy        355 CTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATT 414
              ||| | ||||||  |    || || ||||| || |||||    || |||| |   ||
Db        214 CTACACCCTGGTCCTCACAGACCCCGATGCTCCCAGCAGGAAGGACCCCAAATTCAGGGA 273

Qy        415 CTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCA 474
              |||   || |  |||||     | || ||||||  |||| | |  |  || |   | |
Db        274 GTGGCACCACTTCCTGGTGGTCAACATGAAGGGCAACGACATTAGCAGTGGCACTGTCCT 333

Qy        475 GGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCG 534
              | |  |  |     ||   |       | |    | |   | | |    | ||   |
Db        334 CTCCGAATACGTGGGCTCCGGACCTAAAGACACAGGTCTGCACCGCCGCTACGTCTGGCT 393

Qy        535 CTACCAGTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAA 594
              |      |   | | || | |  | | |    |   |||     ||||
Db        394 GGTGTATGAGCAGGAGCAGCCTCTGAACTGTGACGAGCCCATCCTCAGCAACAAGTCTGG 453

Qy        595 CAAAACTCGAGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACC 654
              | |  || |||   |  ||  ||||    || |  ||    | |||||||| |  ||
Db        454 AGACAACCGCGGCAAGTTCAAGGTGGAGTCCTTCCGCAAGAAGTACCACCTGGGAGCCCC 513

Qy        655 TGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTC 713
              |  ||  ||||    |||  | |  ||    |  |        || |  || || | ||
Db        514 GGTGGCCGGCACGTGCTTCCAGGCAGAGTGGGATGACTCTGTGCCCAAGCTGCATGATC 572
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RESULT 6
US-09-799-451-460
; Sequence 460, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 460
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (125)..(631)
US-09-799-451-460

Query Match 4.6%; Score 41; DB 4; Length 916;
Best Local Similarity 60.2%; Pred. No. 0.01;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Qy        355 CTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATT 414
              ||| | | ||||  ||   || || ||||| || |||||    || |||| | | |||
Db        313 CTACACCTTGGTCCTGACAGACCCGGATGCTCCCAGCAGGAAGGATCCCAAATACAGAGA 372

Qy        415 CTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGA 467
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              |||   ||||  |||||     | || ||||||   ||| | |  |  || |
Db        373 ATGGCATCATTTCCTGGTGGTCAACATGAAGGGCAATGACATCAGCAGTGGCA 425
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RESULT 7
US-08-403-378B-14
; Sequence 14, Application US/08403378B
; Patent No. 5759991
; GENERAL INFORMATION:
; APPLICANT: TOHDOH, NAOKI
; APPLICANT: TOJO, SHIN-ICHIRO
; APPLICANT: KOJIMA, SHIN-ICHI
; APPLICANT: UEKI, YASUYUKI
; APPLICANT: NISHIHARA, TOSHIO
; APPLICANT: FUKUSHIMA, NOBUYUKI
; APPLICANT: IRIE, TSUNEMASA
; APPLICANT: ONO, KEIICHI
; APPLICANT: AGUI, HIDEO
; APPLICANT: OJIKA, KOSEI
; TITLE OF INVENTION: NEUROTROPHIC PEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,378B
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-124688
; FILING DATE: 27-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-080398
; FILING DATE: 30-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-280590
; FILING DATE: 27-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-333241
; FILING DATE: 21-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-243003
; FILING DATE: 12-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,043
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/873,764
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/01214
; FILING DATE: 27-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGART, WADDELL A
; REGISTRATION NUMBER: 24,861
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 base pairs
; TYPE: nucleic acid

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;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       TISSUE TYPE:  placental tissue
;     IMMEDIATE SOURCE:
;       CLONE:  p1-3
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  120..680
;     FEATURE:
;       NAME/KEY:  5'UTR
;       LOCATION:  1..119
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  120..680
;     FEATURE:
;       NAME/KEY:  3'UTR
;       LOCATION:  681..1447
US-08-403-378B-14

  Query Match             4.6%;  Score 41;  DB 1;  Length 1447;
  Best Local Similarity   60.2%;  Pred. No. 0.013;
  Matches   68;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy        355 CTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATT 414
              ||| | | |||| ||   || || ||||| || |||||    || |||| | | |||
Db        308 CTACACCTTGGTCCTGACAGACCCGGATGCTCCCAGCAGGAAGGATCCCAAATACAGAGA 367

Qy        415 CTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGA 467
              |||   ||||  |||||     | || ||||||   ||| | |   |  || |
Db        368 ATGGCATCATTTCCTGGTGGTCAACATGAAGGGCAATGACATCAGCAGTGGCA 420


RESULT 8
US-09-252-991A-2742
; Sequence 2742, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 2742
;   LENGTH: 660
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2742

  Query Match             4.4%;  Score 39;  DB 4;  Length 660;
  Best Local Similarity   47.1%;  Pred. No. 0.037;
  Matches  120;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        604 AGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAG 663
              |||| ||  | || ||  |        ||| |  |||| |  | ||  | | | |
Db        142 AGGCGCTGCGCAACTGTTCGTCGGAACGAATCTTTTCCGGCCAGTCGGCGCGGCTGTACT 201

Qy        664 CACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAG 723
                ||      ||    ||| |   ||||| | ||   || ||   ||||| | |
Db        202 GGCCATAGCGATCGATCAGGCCGGTCAGGATGCTCCGCTCCACCGCCCTCCCTGTGCGTA 261

Qy        724 GGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTT 783
              |||     | || ||||  |  |   | ||| | || ||  ||       | ||||
Db        262 TGCCGAAACGTCCGAGCAGGATGCTCTGGGGAGCTTGCGGCGAGCGCAGGGACAGGCTCA 321

Qy        784 GCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCT 843
              ||  |||| | ||  ||    | ||   || | |||    | |   | | | ||| ||
Db        322 GCGCTCCGACCCTGGCGCGGTCCAGCGAGCCCTCCACGCGTGGCGCCAGCAGCACCCGCT 381

Qy        844 GGATACAGAACCCCT 858
              ||     || |  ||
Db        382 GGCCTTCGACCATCT 396


RESULT 9
US-09-252-991A-3027/c
; Sequence 3027, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 3027
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3027

  Query Match             4.4%;  Score 39;  DB 4;  Length 768;
  Best Local Similarity   47.1%;  Pred. No. 0.041;
  Matches  120;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        604 AGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAG 663
              |||| ||  | || ||  |        ||| |  |||| |  | ||  | | | |
Db        587 AGGCGCTGCGCAACTGTTCGTCGGAACGAATCTTTTCCGGCCAGTCGGCGCGGCTGTACT 528

Qy        664 CACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAG 723
                ||      ||    ||| |   ||||| | ||   || ||   ||||| | |
Db        527 GGCCATAGCGATCGATCAGGCCGGTCAGGATGCTCCGCTCCACCGCCCTCCCTGTGCGTA 468

Qy        724 GGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTT 783
              |||     | || ||||  |  |   | ||| | || ||  ||       | ||||
Db        467 TGCCGAAACGTCCGAGCAGGATGCTCTGGGGAGCTTGCGGCGAGCGCAGGGACAGGCTCA 408

Qy        784 GCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCT 843
              ||  |||| | ||  ||    | ||   || | |||    | |   | | | ||| ||
Db        407 GCGCTCCGACCCTGGCGCGGTCCAGCGAGCCCTCCACGCGTGGCGCCAGCAGCACCCGCT 348

Qy        844 GGATACAGAACCCCT 858
              ||     || |  ||
Db        347 GGCCTTCGACCATCT 333


RESULT 10
US-09-252-991A-2839
; Sequence 2839, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
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;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 2839
;   LENGTH: 1671
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2839

  Query Match             4.4%;  Score 39;  DB 4;  Length 1671;
  Best Local Similarity   47.1%;  Pred. No. 0.068;
  Matches  120;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        604 AGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAG 663
              |||| ||  | || ||  |        ||| |  |||| |  | ||   | |  | |
Db       1326 AGGCGCTGCGCAACTGTTCGTCGGAACGAATCTTTTCCGGCCAGTCGGCGCGGCTGTACT 1385

Qy        664 CACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAG 723
               ||       ||    |||  |   |||||  | ||   || ||   ||||| | |
Db       1386 GGCCATAGCGATCGATCAGGCCGGTCAGGATGCTCCGCTCCACCGCCCTCCCTGTGCGTA 1445

Qy        724 GGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTT 783
              |||      | || ||||  |  |   |  ||| | || ||  ||        | ||||
Db       1446 TGCCGAAACGTCCGAGCAGGATGCTCTGGGGAGCTTGCGGCGAGCGCAGGGACAGGCTCA 1505

Qy        784 GCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCT 843
              ||  ||||  | ||  ||    | ||   ||  | |||    | |   | | | ||| ||
Db       1506 GCGCTCCGACCCTGGCGCGGTCCAGCGAGCCCTCCACGCGTGGCGCCAGCAGCACCCGCT 1565

Qy        844 GGATACAGAACCCCT 858
              ||     || |  ||
Db       1566 GGCCTTCGACCATCT 1580


RESULT 11
US-09-252-991A-3127/c
; Sequence 3127, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 3127
;   LENGTH: 2352
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3127

  Query Match             4.4%;  Score 39;  DB 4;  Length 2352;
  Best Local Similarity   47.1%;  Pred. No. 0.085;
  Matches  120;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        604 AGGCTCTTGGAAAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAG 663
              |||| ||  | || ||  |        ||| |  |||| |  | ||   | |  | |
Db        823 AGGCGCTGCGCAACTGTTCGTCGGAACGAATCTTTTCCGGCCAGTCGGCGCGGCTGTACT 764

Qy        664 CACCCAGTTCATGACCCAGAACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAG 723
               ||       ||    |||  |   |||||  | ||   || ||   ||||| | |
Db        763 GGCCATAGCGATCGATCAGGCCGGTCAGGATGCTCCGCTCCACCGCCCTCCCTGTGCGTA 704

Qy        724 GGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTT 783
              |||      | || ||||  |  |   |  ||| | || ||  ||        | ||||
Db        703 TGCCGAAACGTCCGAGCAGGATGCTCTGGGGAGCTTGCGGCGAGCGCAGGGACAGGCTCA 644

Qy        784 GCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCCTCT 843
              ||  ||||  | ||  ||    | ||   ||  | |||    | |   | | | ||| ||
Db        643 GCGCTCCGACCCTGGCGCGGTCCAGCGAGCCCTCCACGCGTGGCGCCAGCAGCACCCGCT 584

Qy        844 GGATACAGAACCCCT 858
              ||     || |  ||
Db        583 GGCCTTCGACCATCT 569


RESULT 12
US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15639
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15639

  Query Match             4.2%;  Score 37.8;  DB 4;  Length 505;
  Best Local Similarity   13.5%;  Pred. No. 0.078;
  Matches   58;  Conservative  179;  Mismatches  191;  Indels    3;  Gaps    1;

Qy         97 GACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGA 156
              || ||::: :: |:  |||:    : :|  :   ::   || |:||::|::   :: :|:
Db        432 GAGAAWKRWKMAGSMRACARAGTTMAWGACWAMARRGWRCARGRTGSWGSWKGGYRMWGR 373

Qy        157 CGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTG 216
                 |    :: ||  |::||     :  :  |:  :  : :::  :|: : :::||:| :
Db        372 GMAAAKMRRMAAAGGSYCGMTSYTSGSKMTGRKGSMTKRKRMMTYSGMWWTSYKCTKTGK 313

Qy        217 CCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACATTGGC---TGCAAGGTTGTTCC 273
               : | :: :|::  | :  :: :: |    : :::|  ::: :    : |: :    ::
Db        312 KYTGWKSKKTRWTCTSWRKYMWMMSGCWARSMKSWARSWYSMMACWCMMSASAYRARRSM 253

Qy        274 TGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCC 333
              :||  : ::  | :: |::  ::|: :: :: :  :::  :||  :: :::::    :::
Db        252 YGARRSMMRAGAGWWRARRGKKRARGKSSMMRSKMSSMRMSAGKARMCRRWMWSCRRMSY 193

Qy        334 GGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGATGCCCCTAGCAG 393
              :  |: |  :       :  :|::: :  |: : |       ||:::|:: :  :: |
Db        192 SCMGSKCMSCRGTCAKMWRYARYAKRYASSMGKYMMGCRWCYAKCARMYGYYRSRSRSTG 133

Qy        394 AGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAACAGATATCAAGGGCGCCGA 453
               : :: :   :  :::  ::  :  :   | :| : : ::::|:: |  : :: ::::::
Db        132 SRGMKYRRRKMYYMWKYWMWSWWCYRMGAAMYGMSARAYRMYASMSACKMCSRMMKMMSW 73

Qy        454 CCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACC 513
              ::: :  : : : ::: ::| :   :  :|    :|:     :  :: :: : | :: ::
Db         72 SMWMRCWRSRYRCWMSGKWCYSCCGYCCSACRMCYCWTRRMKSWYSSRKSRMCCRYMSMS 13

Qy        514 GGCACACAGTG 524
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Db         12 SAYRYSSKRTK 2


RESULT 13
US-09-949-016-29
; Sequence 29, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
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;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 2441
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-29

  Query Match             4.2%;  Score 37.6;  DB 4;  Length 2441;
  Best Local Similarity   44.6%;  Pred. No. 0.25;
  Matches  148;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy         75 AACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTGTTACTGGGTC 134
              |||||  | | ||||  | | ||| |  ||   |   ||   |   ||      |||  |
Db       1984 AACCATGGCTCCCCACAGCTGGGAGAGGGAATGTTCCCAGCACCAGACCTCCCGTGGCCC 2043

Qy        135 TCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCT 194
               |  |  |||||||   | |  | |     | |   |||  |    |||  ||   ||||
Db       2044 ACCAGCCTGTGGTCAGCAGTGTGGGGCCCCAAACTGGCCTGCAGTCCCCTGGCACCCTTC 2103

Qy        195 TGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGGGGAACA 254
               |  |   ||   |||||  |  || ||| |  |||   |||| ||      |  | | ||
Db       2104 AGCCCCCTGAGTTCCTCTACTCTCATGGCGTGCAAGGACTCTATCCCCTCATCAGTACCA 2163

Qy        255 TTGGCTGCAAGGTTGTTCCTGATTGTAACAACTACAGACAGAAGATCACCTCCTGGATGG 314
               |   |||| ||   |  |    || |     |  ||||  || | |  |   |  ||
Db       2164 CTCTGTGCACGGAGTTGGCATGGTGCAGAGTGGAGCGACAATAGCTAAAGTGAGGCCTGC 2223

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
               |  |       | ||||  | |   | |   |    |    | |    |   | | |
Db       2224 TTCACAACAGACATTTCCTAGAGAAAGAGAGAGAGAGAGGAGAAAGAGAGAGAAGGAGAG 2283

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGA 406
              |  |||  |||   || |   || |  | |||
Db       2284 AGACAGTAGCCAAGAGAACCCCACAGACAAGA 2315


RESULT 14
US-09-060-726A-1
; Sequence 1, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
;  APPLICANT:  Weigel, Detlef
;  APPLICANT:  Salk Institute
;  TITLE OF INVENTION:  FLOWERING LOCUS T (FT) AND GENETICALLY
;  TITLE OF INVENTION:  MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
;  FILE REFERENCE:  SALKINS.026A
;  CURRENT APPLICATION NUMBER: US/09/060,726A
;  CURRENT FILING DATE:  1998-04-15
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 855
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (63)...(590)
US-09-060-726A-1

  Query Match             4.1%;  Score 36.8;  DB 3;  Length 855;
  Best Local Similarity   55.5%;  Pred. No. 0.23;
  Matches   71;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
              |||| | |||  || |    || |  |    | |      |||||   |||| |||||||
Db        214 AGCCAAGAGTTGAGATTGGTGGAGAAGACCTCAGGAACTTCTATACTTTGGTTATGGTGG 273

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              |||||||||  || ||         | ||     |   ||   |     |||||| |||| |
Db        274 ATCCAGATGTTCCAAGTCCTAGCAACCCTCACCTCCGAGAATATCTCCATTGGTTGGTGA 333

Qy        435 CAGATATC 442
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Db        334 CTGATATC 341


RESULT 15
US-09-060-726A-3/c
; Sequence 3, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
;  APPLICANT:  Weigel, Detlef
;  APPLICANT:  Salk Institute
;  TITLE OF INVENTION:  FLOWERING LOCUS T (FT) AND GENETICALLY
;  TITLE OF INVENTION:  MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
;  FILE REFERENCE:  SALKINS.026A
;  CURRENT APPLICATION NUMBER: US/09/060,726A
;  CURRENT FILING DATE:  1998-04-15
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 856
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-060-726A-3

  Query Match             4.1%;  Score 36.8;  DB 3;  Length 856;
  Best Local Similarity   55.5%;  Pred. No. 0.23;
  Matches   71;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy        315 AGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGG 374
              |||| | |||  || |    || |  |    | |      |||||   |||| |||||||
Db        643 AGCCAAGAGTTGAGATTGGTGGAGAAGACCTCAGGAACTTCTATACTTTGGTTATGGTGG 584

Qy        375 ATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA 434
              |||||||||  || ||         | ||     |   ||   |     |||||| |||| |
Db        583 ATCCAGATGTTCCAAGTCCTAGCAACCCTCACCTCCGAGAATATCTCCATTGGTTGGTGA 524

Qy        435 CAGATATC 442
              | ||||||
Db        523 CTGATATC 516


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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

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Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
9	890	100.0	890	14	US-10-036-160-60	Sequence 60, Appl
53	890	100.0	890	15	US-10-223-085-305	Sequence 305, App
59	890	100.0	890	15	US-10-219-065-231	Sequence 231, App
85	890	100.0	890	15	US-10-223-084-305	Sequence 305, App
86	890	100.0	890	15	US-10-223-088-305	Sequence 305, App
87	890	100.0	890	15	US-10-223-090-305	Sequence 305, App
92	890	100.0	890	15	US-10-223-087-305	Sequence 305, App
93	890	100.0	890	15	US-10-223-083-305	Sequence 305, App
96	890	100.0	890	15	US-10-223-089-305	Sequence 305, App
99	890	100.0	890	16	US-10-223-081-305	Sequence 305, App
118	890	100.0	890	16	US-10-223-082-305	Sequence 305, App
119	890	100.0	890	17	US-10-305-654-305	Sequence 305, App
122	890	100.0	890	18	US-10-081-056-305	Sequence 305, App
127	890	100.0	890	20	US-10-884-091-60	Sequence 60, Appl
128	874.8	98.3	972	17	US-10-291-265-9	Sequence 9, Appli
129	865.2	97.2	932	13	US-10-003-152-1	Sequence 1, Appli
130	865.2	97.2	932	14	US-10-002-050-1	Sequence 1, Appli
131	865.2	97.2	932	14	US-10-002-304-1	Sequence 1, Appli
132	865.2	97.2	932	17	US-10-403-676-57	Sequence 57, Appl
133	858.4	96.4	903	10	US-09-879-401-4	Sequence 4, Appli
134	835.2	93.8	879	17	US-10-403-676-75	Sequence 75, Appl
135	833.2	93.6	1028	10	US-09-895-298-56	Sequence 56, Appl
136	833.2	93.6	1028	20	US-10-885-039-56	Sequence 56, Appl
137	832.8	93.6	876	19	US-10-403-142-127	Sequence 127, App
138	832.8	93.6	876	19	US-10-403-142-129	Sequence 129, App
139	831.2	93.4	876	19	US-10-403-142-107	Sequence 107, App
140	829.6	93.2	876	19	US-10-403-142-117	Sequence 117, App
141	829.6	93.2	876	19	US-10-403-142-119	Sequence 119, App
142	829.6	93.2	876	19	US-10-403-142-121	Sequence 121, App
143	829.6	93.2	876	19	US-10-403-142-123	Sequence 123, App
144	829.6	93.2	876	19	US-10-403-142-125	Sequence 125, App
145	801.8	90.1	952	10	US-09-895-298-61	Sequence 61, Appl
146	801.8	90.1	952	20	US-10-885-039-61	Sequence 61, Appl
147	785.4	88.2	886	17	US-10-291-265-481	Sequence 481, App
148	783.8	88.1	826	11	US-09-978-360A-183	Sequence 183, App
149	783.8	88.1	826	21	US-10-926-683-7	Sequence 7, Appli
150	666.2	74.9	706	17	US-10-403-676-61	Sequence 61, Appl
151	664.6	74.7	706	17	US-10-403-676-59	Sequence 59, Appl
152	610.2	68.6	615	14	US-10-116-802-409	Sequence 409, App
153	598.2	67.2	615	17	US-10-403-676-77	Sequence 77, Appl
154	598.2	67.2	627	19	US-10-403-142-113	Sequence 113, App
155	598.2	67.2	634	17	US-10-403-676-69	Sequence 69, Appl
156	596.6	67.0	627	19	US-10-403-142-109	Sequence 109, App
157	596.6	67.0	634	17	US-10-403-676-67	Sequence 67, Appl
158	595.6	66.9	619	17	US-10-403-676-65	Sequence 65, Appl
159	593.4	66.7	627	19	US-10-403-142-111	Sequence 111, App
160	593.4	66.7	627	19	US-10-403-142-115	Sequence 115, App
161	592.4	66.6	619	17	US-10-403-676-63	Sequence 63, Appl
162	527.6	59.3	547	17	US-10-403-676-71	Sequence 71, Appl
163	526	59.1	547	17	US-10-403-676-73	Sequence 73, Appl
164	297.2	33.4	429	10	US-09-918-995-5859	Sequence 5859, Ap
165	270.2	30.4	294	20	US-10-425-115-127514	Sequence 127514,
c 166	164.2	18.4	303	16	US-10-257-826A-301	Sequence 301, App
167	49.8	5.6	1199	18	US-10-425-114-15850	Sequence 15850, A
168	48.2	5.4	1191	21	US-10-343-477A-17	Sequence 17, Appl
169	48.2	5.4	1338	20	US-10-425-115-58988	Sequence 58988, A
170	47.2	5.3	1078	21	US-10-343-477A-7	Sequence 7, Appli
171	47.2	5.3	1105	18	US-10-425-114-15835	Sequence 15835, A
172	47	5.3	1037	16	US-10-316-253-106	Sequence 106, App
173	47	5.3	1075	16	US-10-316-253-104	Sequence 104, App
174	46.2	5.2	886	21	US-10-343-477A-43	Sequence 43, Appl
175	46	5.2	558	19	US-10-437-963-46503	Sequence 46503, A
176	45.6	5.1	836	19	US-10-767-701-20360	Sequence 20360, A
177	45.4	5.1	847	18	US-10-432-531-23	Sequence 23, Appl
178	45.4	5.1	847	18	US-10-432-531-24	Sequence 24, Appl
179	45.4	5.1	1212	19	US-10-437-963-65873	Sequence 65873, A
180	44.2	5.0	339	19	US-10-437-963-33008	Sequence 33008, A
181	42.8	4.8	398	9	US-09-960-352-12904	Sequence 12904, A
182	42.8	4.8	425	9	US-09-960-352-9788	Sequence 9788, Ap
183	42.8	4.8	441	9	US-09-960-352-11931	Sequence 11931, A
c 184	42.8	4.8	459	9	US-09-960-352-2118	Sequence 2118, Ap
185	42.2	4.7	842	19	US-10-655-799-6	Sequence 6, Appli
186	41.2	4.6	510	19	US-10-437-963-36212	Sequence 36212, A
187	41	4.6	428	10	US-09-918-995-3240	Sequence 3240, Ap
188	41	4.6	431	10	US-09-918-995-17430	Sequence 17430, A
189	41	4.6	474	10	US-09-918-995-30756	Sequence 30756, A
190	41	4.6	485	10	US-09-918-995-32278	Sequence 32278, A
191	41	4.6	486	10	US-09-918-995-27695	Sequence 27695, A
192	41	4.6	564	20	US-10-873-595-57	Sequence 57, Appl
193	41	4.6	576	10	US-09-918-995-26543	Sequence 26543, A
194	41	4.6	831	20	US-10-491-733-43	Sequence 43, Appl

	195	41	4.6	916	18	US-10-302-172-460 Sequence 460, App
	196	41	4.6	1079	18	US-10-363-616-37 Sequence 37, Appl
	197	41	4.6	1400	21	US-10-956-157-6104 Sequence 6104, Ap
	198	41	4.6	1434	20	US-10-851-921-9 Sequence 9, Appli
	199	41	4.6	1444	9	US-09-960-253-167 Sequence 167, App
	200	41	4.6	1444	9	US-09-880-107-3790 Sequence 3790, Ap
	201	41	4.6	1444	15	US-10-171-581-15 Sequence 15, Appl
	202	41	4.6	1444	21	US-10-956-157-869 Sequence 869, App
	203	41	4.6	1732	20	US-10-357-930-29458 Sequence 29458, A
	204	40.8	4.6	837	21	US-10-343-477A-15 Sequence 15, Appl
	205	40.8	4.6	853	18	US-10-425-114-25107 Sequence 25107, A
	206	40.8	4.6	1111	20	US-10-425-115-105835 Sequence 105835,
	207	40.6	4.6	599	21	US-10-487-901-3299 Sequence 3299, Ap
	208	40.6	4.6	610	21	US-10-487-901-6944 Sequence 6944, Ap
	209	40	4.5	400	17	US-10-242-535A-8371 Sequence 8371, Ap
	210	40	4.5	400	18	US-10-085-783A-8371 Sequence 8371, Ap
	211	40	4.5	855	18	US-10-424-599-99933 Sequence 99933, A
c	212	39.8	4.5	856	20	US-10-425-115-142166 Sequence 142166,
	213	39.6	4.4	424	9	US-09-960-352-5143 Sequence 5143, Ap
	214	39.6	4.4	528	9	US-09-938-842A-2635 Sequence 2635, Ap
	215	39.6	4.4	528	11	US-09-938-842A-2635 Sequence 2635, Ap
	216	38.6	4.3	189	17	US-10-382-970-9 Sequence 9, Appli
	217	38.6	4.3	189	19	US-10-384-435B-9 Sequence 9, Appli
	218	38.4	4.3	358	9	US-09-983-965-2772 Sequence 2772, Ap
	219	38	4.3	734	20	US-10-425-115-76582 Sequence 76582, A
	220	38	4.3	1137	18	US-10-425-114-27955 Sequence 27955, A
	221	37.8	4.2	492	21	US-10-343-477A-1 Sequence 1, Appli
	222	37.8	4.2	825	19	US-10-655-799-7 Sequence 7, Appli
	223	37.8	4.2	866	19	US-10-437-963-70271 Sequence 70271, A
c	224	37.8	4.2	1193	17	US-10-282-122A-11679 Sequence 11679, A
	225	37.8	4.2	219352	19	US-10-322-281-45 Sequence 45, Appl
	226	37	4.2	635	18	US-10-424-599-132133 Sequence 132133,
	227	36.8	4.1	831	10	US-09-919-478-1 Sequence 1, Appli
	228	36.8	4.1	856	9	US-09-291-809C-1 Sequence 1, Appli
c	229	36.8	4.1	856	9	US-09-291-809C-3 Sequence 3, Appli
	230	36.8	4.1	856	9	US-09-845-849-1 Sequence 1, Appli
c	231	36.8	4.1	856	9	US-09-845-849-3 Sequence 3, Appli
	232	36.4	4.1	851	20	US-10-653-047-6489 Sequence 6489, Ap
	233	36.4	4.1	1004	21	US-10-343-477A-59 Sequence 59, Appl
	234	36.4	4.1	1554	17	US-10-369-493-40603 Sequence 40603, A
	235	36.2	4.1	732	17	US-10-262-445-27 Sequence 27, Appl
	236	36	4.0	2718	20	US-10-738-986-15 Sequence 15, Appl
	237	35.8	4.0	649	18	US-10-425-114-7785 Sequence 7785, Ap
	238	35.8	4.0	1051	18	US-10-424-599-38496 Sequence 38496, A
	239	35.6	4.0	717	13	US-10-027-632-160181 Sequence 160181,
	240	35.6	4.0	717	17	US-10-027-632-160181 Sequence 160181,
c	241	35.4	4.0	1049	14	US-10-123-155-358 Sequence 358, App
	254	35.2	4.0	775	18	US-10-425-114-26592 Sequence 26592, A
	255	35.2	4.0	790	19	US-10-437-963-67035 Sequence 67035, A
	256	35.2	4.0	1226	21	US-10-343-477A-29 Sequence 29, Appl
c	257	35.2	4.0	4420	19	US-10-437-963-89872 Sequence 89872, A
	258	35.2	4.0	251364	14	US-10-175-523-58 Sequence 58, Appl
	259	35.2	4.0	251364	14	US-10-175-523-61 Sequence 61, Appl
	260	35.2	4.0	251364	14	US-10-175-523-79 Sequence 79, Appl
c	261	34.8	3.9	411	21	US-10-487-901-3805 Sequence 3805, Ap
c	262	34.8	3.9	647	20	US-10-425-115-15971 Sequence 15971, A
	263	34.8	3.9	1383	18	US-10-417-700A-120 Sequence 120, App
	264	34.6	3.9	277	20	US-10-425-115-39337 Sequence 39337, A
	267	34.6	3.9	1482	17	US-10-369-493-44139 Sequence 44139, A
	268	34.6	3.9	15690	21	US-10-312-052B-1 Sequence 1, Appli
	269	34.6	3.9	15690	21	US-10-312-052B-2 Sequence 2, Appli
	270	34.6	3.9	18826	21	US-10-312-052B-3 Sequence 3, Appli
	271	34.6	3.9	21936	21	US-10-741-600-18000 Sequence 18000, A
	272	34.4	3.9	522	19	US-10-437-963-58134 Sequence 58134, A
	273	34.4	3.9	613	21	US-10-343-477A-53 Sequence 53, Appl
	274	34.2	3.8	426	9	US-09-960-352-13608 Sequence 13608, A
	275	34.2	3.8	782	18	US-10-425-114-28494 Sequence 28494, A
	276	34.2	3.8	793	18	US-10-424-599-139104 Sequence 139104,
	277	34.2	3.8	850	21	US-10-343-477A-35 Sequence 35, Appl
	278	34.2	3.8	880	20	US-10-425-115-26387 Sequence 26387, A
	279	34.2	3.8	927	20	US-10-425-115-171729 Sequence 171729,
	280	34.2	3.8	2851	18	US-10-424-599-98687 Sequence 98687, A
	281	34.2	3.8	3735	17	US-10-369-493-44134 Sequence 44134, A
	282	34.2	3.8	149430	21	US-10-626-832-1 Sequence 1, Appli
	283	34.2	3.8	150223	19	US-10-624-149A-1 Sequence 1, Appli
c	284	34	3.8	13606	14	US-10-239-676-166 Sequence 166, App
c	285	34	3.8	13606	15	US-10-311-455-1784 Sequence 1784, Ap
c	286	34	3.8	13606	15	US-10-240-453-188 Sequence 188, App
c	287	34	3.8	13606	18	US-10-221-714A-284 Sequence 284, App
c	288	33.8	3.8	397	18	US-10-424-599-88187 Sequence 88187, A
	289	33.6	3.8	426	9	US-09-960-352-1964 Sequence 1964, Ap
	290	33.6	3.8	570	19	US-10-767-701-20565 Sequence 20565, A
c	291	33.6	3.8	667	21	US-10-486-706-244 Sequence 244, App
	292	33.6	3.8	856	19	US-10-767-701-7965 Sequence 7965, Ap
c	293	33.6	3.8	1054	18	US-10-424-599-73702 Sequence 73702, A
	294	33.6	3.8	1153	18	US-10-424-599-39694 Sequence 39694, A
	295	33.6	3.8	1184	14	US-10-123-155-412 Sequence 412, App
c	308	33.6	3.8	1606	9	US-09-820-004-1 Sequence 1, Appli
c	309	33.6	3.8	1606	19	US-10-644-021A-1 Sequence 1, Appli
	310	33.6	3.8	1644	18	US-10-152-319A-2202 Sequence 2202, Ap
c	311	33.6	3.8	2097	16	US-10-240-965-172 Sequence 172, App
c	312	33.6	3.8	2097	22	US-10-765-700-30 Sequence 30, Appl
c	313	33.6	3.8	2884	17	US-10-108-260A-2232 Sequence 2232, Ap
	314	33.4	3.8	1017	20	US-10-739-930-4699 Sequence 4699, Ap
c	315	33.4	3.8	352938	19	US-10-322-696-79 Sequence 79, Appl
	316	33.2	3.7	325	9	US-09-783-590-2932 Sequence 2932, Ap
	317	33.2	3.7	405	10	US-09-918-995-6737 Sequence 6737, Ap
	318	33.2	3.7	409	10	US-09-918-995-6640 Sequence 6640, Ap
	319	33.2	3.7	411	10	US-09-918-995-6913 Sequence 6913, Ap
	320	33.2	3.7	420	10	US-09-918-995-7012 Sequence 7012, Ap
	321	33.2	3.7	590	17	US-10-187-975-51 Sequence 51, Appl
	322	33.2	3.7	616	13	US-10-074-247-1 Sequence 1, Appli
c	323	33.2	3.7	854	20	US-10-478-914-7 Sequence 7, Appli
	324	33.2	3.7	899	21	US-10-343-477A-11 Sequence 11, Appl
	325	33.2	3.7	926	9	US-09-925-302-39 Sequence 39, Appl
	326	33.2	3.7	926	10	US-09-925-302-39 Sequence 39, Appl
	327	33.2	3.7	1617	19	US-10-437-963-33676 Sequence 33676, A
	328	33.2	3.7	1641	14	US-10-153-668-429 Sequence 429, App
	329	33.2	3.7	1762	14	US-10-153-668-317 Sequence 317, App
	330	33.2	3.7	1762	14	US-10-175-523-14 Sequence 14, Appl
	331	33.2	3.7	2588	9	US-09-822-830A-47 Sequence 47, Appl
	332	33.2	3.7	2653	17	US-10-159-563-141 Sequence 141, App
	333	33.2	3.7	3586	21	US-10-764-420-1538 Sequence 1538, Ap
	334	33	3.7	627	17	US-10-369-493-37694 Sequence 37694, A
	335	33	3.7	722	13	US-10-027-632-117446 Sequence 117446,
	336	33	3.7	722	17	US-10-027-632-117446 Sequence 117446,
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c	338	33	3.7	850	13	US-10-027-632-158349 Sequence 158349,
c	339	33	3.7	850	17	US-10-027-632-158348 Sequence 158348,
c	340	33	3.7	850	17	US-10-027-632-158349 Sequence 158349,
	341	33	3.7	1012	18	US-10-424-599-58257 Sequence 58257, A
c	342	33	3.7	1249	19	US-10-437-963-30347 Sequence 30347, A
c	343	33	3.7	1386	15	US-10-156-761-1853 Sequence 1853, Ap
c	344	33	3.7	1901	20	US-10-425-115-164827 Sequence 164827,
c	345	33	3.7	3015	19	US-10-437-963-41677 Sequence 41677, A
c	346	33	3.7	9025608	15	US-10-156-761-1 Sequence 1, Appli
c	347	32.8	3.7	226	14	US-10-060-036-1476 Sequence 1476, Ap
	348	32.8	3.7	441	10	US-09-764-891-2503 Sequence 2503, Ap
	349	32.8	3.7	725	20	US-10-425-115-158568 Sequence 158568,
c	350	32.8	3.7	781	19	US-10-656-269-3 Sequence 3, Appli
c	351	32.8	3.7	970	19	US-10-656-269-1 Sequence 1, Appli
c	352	32.8	3.7	1278	20	US-10-481-698-57 Sequence 57, Appl
	353	32.8	3.7	1298	20	US-10-425-115-153284 Sequence 153284,
c	354	32.8	3.7	1413	9	US-09-728-952-36 Sequence 36, Appl
	355	32.8	3.7	1932	20	US-10-425-115-6938 Sequence 6938, Ap
c	356	32.8	3.7	2199	17	US-10-094-749-1302 Sequence 1302, Ap
	357	32.8	3.7	2429	14	US-10-198-846-14054 Sequence 14054, A
	358	32.8	3.7	2849	21	US-10-764-420-501 Sequence 501, App
c	805	32.8	3.7	3479	21	US-10-931-886-123 Sequence 123, App
	807	32.8	3.7	9905	14	US-10-270-144-3 Sequence 3, Appli
c	808	32.8	3.7	10561	19	US-10-656-269-18 Sequence 18, Appl
c	809	32.8	3.7	11006	19	US-10-656-269-17 Sequence 17, Appl
	810	32.8	3.7	13886	21	US-10-741-600-17592 Sequence 17592, A
c	811	32.8	3.7	15065	21	US-10-741-600-17874 Sequence 17874, A
c	812	32.6	3.7	201	20	US-10-719-993-19255 Sequence 19255, A
	813	32.6	3.7	201	20	US-10-719-993-53580 Sequence 53580, A

c 814	32.6	3.7	201	21	US-10-741-600-39090	Sequence 39090, A
815	32.6	3.7	201	21	US-10-741-600-71058	Sequence 71058, A
816	32.6	3.7	298	21	US-10-487-901-3301	Sequence 3301, Ap
c 817	32.6	3.7	406	20	US-10-357-930-60859	Sequence 60859, A
818	32.6	3.7	627	18	US-10-425-114-18069	Sequence 18069, A
819	32.6	3.7	866	18	US-10-425-114-25385	Sequence 25385, A
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821	32.6	3.7	907	19	US-10-437-963-19262	Sequence 19262, A
822	32.6	3.7	1167	20	US-10-425-115-103681	Sequence 103681,
823	32.6	3.7	1260	17	US-10-282-122A-15071	Sequence 15071, A
824	32.6	3.7	4240	20	US-10-425-115-90868	Sequence 90868, A
825	32.6	3.7	70210	20	US-10-719-993-7063	Sequence 7063, Ap
826	32.6	3.7	70210	21	US-10-741-600-17994	Sequence 17994, A
c 827	32.6	3.7	1980090	20	US-10-719-993-6815	Sequence 6815, Ap
c 828	32.6	3.7	1980090	21	US-10-741-600-17676	Sequence 17676, A
829	32.6	3.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 830	32.4	3.6	231	19	US-10-437-963-63877	Sequence 63877, A
c 831	32.4	3.6	509	14	US-10-123-155-108	Sequence 108, App
c 844	32.4	3.6	747	15	US-10-156-761-3070	Sequence 3070, Ap
845	32.4	3.6	796	19	US-10-767-701-19794	Sequence 19794, A
c 846	32.4	3.6	201143	18	US-10-240-425-1099	Sequence 1099, Ap
847	32.2	3.6	380	9	US-09-960-352-12191	Sequence 12191, A
850	32.2	3.6	865	18	US-10-425-114-31743	Sequence 31743, A
c 851	32.2	3.6	980	17	US-10-260-238-5103	Sequence 5103, Ap
852	32.2	3.6	1678	18	US-10-425-114-32574	Sequence 32574, A
853	32.2	3.6	1678	20	US-10-425-115-97380	Sequence 97380, A
854	32.2	3.6	1821	19	US-10-437-963-55247	Sequence 55247, A
855	32.2	3.6	3481	18	US-10-425-114-32821	Sequence 32821, A
856	32.2	3.6	3665	20	US-10-425-115-97384	Sequence 97384, A
c 857	32.2	3.6	32659	17	US-10-085-117-208	Sequence 208, App
858	32.2	3.6	49888	17	US-10-085-117-25	Sequence 25, Appl
c 859	32	3.6	338	20	US-10-357-930-23224	Sequence 23224, A
c 860	32	3.6	338	20	US-10-357-930-29096	Sequence 29096, A
861	32	3.6	341	20	US-10-357-930-5099	Sequence 5099, Ap
862	32	3.6	342	20	US-10-357-930-14268	Sequence 14268, A
863	32	3.6	394	20	US-10-357-930-35388	Sequence 35388, A
864	32	3.6	394	20	US-10-357-930-44220	Sequence 44220, A
c 865	32	3.6	598	13	US-10-027-632-193091	Sequence 193091,
c 866	32	3.6	598	17	US-10-027-632-193091	Sequence 193091,
c 867	32	3.6	1320	18	US-10-641-643-1248	Sequence 1248, Ap
c 868	32	3.6	1349	18	US-10-287-226-99	Sequence 99, Appl
c 869	32	3.6	1617	19	US-10-437-963-101417	Sequence 101417,
c 870	32	3.6	1649	17	US-10-159-563-264	Sequence 264, App
c 871	32	3.6	1649	19	US-10-304-125-4	Sequence 4, Appli
c 872	32	3.6	1743	16	US-10-133-013-219	Sequence 219, App
c 873	32	3.6	1900	20	US-10-357-930-22804	Sequence 22804, A
c 874	32	3.6	1900	20	US-10-357-930-28658	Sequence 28658, A
c 875	32	3.6	2051	19	US-10-304-125-13	Sequence 13, Appl
c 876	32	3.6	2345	19	US-10-437-963-28165	Sequence 28165, A
c 877	31.8	3.6	139	21	US-10-486-706-403	Sequence 403, App
878	31.8	3.6	389	20	US-10-425-115-89481	Sequence 89481, A
879	31.8	3.6	774	15	US-10-156-761-6275	Sequence 6275, Ap
880	31.8	3.6	777	15	US-10-156-761-1644	Sequence 1644, Ap
c 881	31.8	3.6	1020	15	US-10-217-335-12	Sequence 12, Appl
c 882	31.8	3.6	2015	10	US-09-870-089B-1	Sequence 1, Appli
c 883	31.8	3.6	2015	17	US-10-341-434-66	Sequence 66, Appl
c 884	31.8	3.6	2015	17	US-10-172-118-647	Sequence 647, App
c 885	31.8	3.6	2015	17	US-10-262-445-116	Sequence 116, App
c 886	31.8	3.6	2015	18	US-10-342-887-647	Sequence 647, App
c 887	31.8	3.6	2015	19	US-10-283-975A-141	Sequence 141, App
c 888	31.8	3.6	2015	20	US-10-370-715B-641	Sequence 641, App
c 889	31.8	3.6	2015	21	US-10-813-859-1	Sequence 1, Appli
c 890	31.8	3.6	2015	21	US-10-956-157-664	Sequence 664, App
c 891	31.8	3.6	2019	10	US-09-919-039-173	Sequence 173, App
892	31.8	3.6	2490	17	US-10-108-260A-200	Sequence 200, App
893	31.8	3.6	2583	19	US-10-441-926-31	Sequence 31, Appl
894	31.8	3.6	2583	19	US-10-441-926-32	Sequence 32, Appl
895	31.8	3.6	2583	19	US-10-441-926-33	Sequence 33, Appl
896	31.8	3.6	42794	21	US-10-741-600-17670	Sequence 17670, A
c 897	31.8	3.6	71292	13	US-10-087-192-1942	Sequence 1942, Ap
898	31.6	3.6	404	10	US-09-918-995-6244	Sequence 6244, Ap
899	31.6	3.6	496	10	US-09-918-995-20527	Sequence 20527, A
900	31.6	3.6	501	20	US-10-425-115-35543	Sequence 35543, A
c 901	31.6	3.6	619	13	US-10-027-632-108752	Sequence 108752,
c 902	31.6	3.6	619	17	US-10-027-632-108752	Sequence 108752,
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904	31.6	3.6	635	17	US-10-027-632-46181	Sequence 46181, A
c 905	31.6	3.6	638	16	US-10-029-386-22749	Sequence 22749, A
c 906	31.6	3.6	800	18	US-10-425-114-17366	Sequence 17366, A
907	31.6	3.6	1042	17	US-10-187-975-49	Sequence 49, Appl
908	31.6	3.6	1354	20	US-10-425-115-102049	Sequence 102049,
c 909	31.6	3.6	1360	9	US-09-764-853-234	Sequence 234, App
c 910	31.6	3.6	1391	20	US-10-425-115-7205	Sequence 7205, Ap
c 911	31.6	3.6	1874	9	US-09-323-998D-33	Sequence 33, Appl
912	31.6	3.6	2167	17	US-10-264-237-1332	Sequence 1332, Ap
913	31.6	3.6	2961	10	US-09-822-846-168	Sequence 168, App
914	31.6	3.6	2991	9	US-09-729-674-155	Sequence 155, App
915	31.6	3.6	2991	21	US-10-913-553-155	Sequence 155, App
916	31.6	3.6	3335	17	US-10-191-803-50	Sequence 50, Appl
917	31.6	3.6	3335	18	US-10-152-319A-1573	Sequence 1573, Ap
918	31.6	3.6	3335	21	US-10-486-706-202	Sequence 202, App
c 919	31.6	3.6	3843	17	US-10-108-260A-1691	Sequence 1691, Ap
920	31.6	3.6	6949	20	US-10-723-860-2112	Sequence 2112, Ap
921	31.6	3.6	7066	20	US-10-723-860-6378	Sequence 6378, Ap
c 922	31.6	3.6	15297	13	US-10-003-295-3	Sequence 3, Appli
c 923	31.6	3.6	15297	18	US-10-660-763-3	Sequence 3, Appli
c 924	31.6	3.6	26433	21	US-10-741-600-17625	Sequence 17625, A
c 925	31.6	3.6	34551	15	US-10-017-161-2231	Sequence 2231, Ap
c 926	31.6	3.6	34551	17	US-10-292-798-1877	Sequence 1877, Ap
c 927	31.6	3.6	95683	13	US-10-087-192-160	Sequence 160, App
928	31.6	3.6	96589	11	US-09-997-722-46	Sequence 46, Appl
929	31.6	3.6	241805	19	US-10-741-601-5621	Sequence 5621, Ap
930	31.6	3.6	241805	21	US-10-741-600-17581	Sequence 17581, A
c 931	31.6	3.6	350764	13	US-10-087-192-1864	Sequence 1864, Ap
c 932	31.4	3.5	497	19	US-10-767-701-6629	Sequence 6629, Ap
933	31.4	3.5	625	14	US-10-123-155-70	Sequence 70, Appl
c 946	31.4	3.5	721	20	US-10-425-115-6244	Sequence 6244, Ap
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948	31.4	3.5	750	9	US-09-834-759-58	Sequence 58, Appl
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953	31.4	3.5	750	16	US-10-124-805-58	Sequence 58, Appl
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964	31.4	3.5	1871	17	US-10-027-632-263807	Sequence 263807,
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967	31.4	3.5	2787	19	US-10-793-639-203	Sequence 203, App
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983	31.2	3.5	1437	17	US-10-359-369-17	Sequence 17, Appl
984	31.2	3.5	1437	21	US-10-688-745-65	Sequence 65, Appl
985	31.2	3.5	1771	20	US-10-425-115-98208	Sequence 98208, A

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988	31.2	3.5	2583	19	US-10-441-926-39	Sequence 39, Appl
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995	31.2	3.5	176080	18	US-10-235-192A-43	Sequence 43, Appl
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c 998	31	3.5	31	14	US-10-002-304-37	Sequence 37, Appl
c 999	31	3.5	31	17	US-10-403-676-154	Sequence 154, App
c1000	31	3.5	31	19	US-10-403-142-223	Sequence 223, App
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1015	31	3.5	790	17	US-10-027-632-160894	Sequence 160894,
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1019	31	3.5	1191	18	US-10-425-114-4721	Sequence 4721, Ap
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1023	31	3.5	1385	19	US-10-437-963-64591	Sequence 64591, A
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1492	31	3.5	4277	15	US-10-223-084-157	Sequence 157, App
1493	31	3.5	4277	15	US-10-223-088-157	Sequence 157, App
1494	31	3.5	4277	15	US-10-223-090-157	Sequence 157, App
1495	31	3.5	4277	15	US-10-223-087-157	Sequence 157, App

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